

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 12, 2004, 09:59:06 ; Search time 41 Seconds

(without alignments)  
30.971 Million cell updates/sec

Title: US-09-185-908-1

Perfect score: 23

Sequence: 1 WXXXXXXG 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 561297

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq 19Jun03.\*

```
1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	16	69.6	17	ABB07407	xynA fragment in p
2	16	69.6	20	AA178408	Human papillomavir
3	16	69.6	20	ABB07406	xynA fragment in p
4	16	69.6	32	AA138243	Human secreted pro
5	16	69.6	33	AA144053	Mutant hCS peptide
6	15	65.2	10	AAG4992	Human complementar
7	15	65.2	10	AAG4994	Human complementar
8	15	65.2	13	AAW86105	Peptide from human
9	15	65.2	13	AAW86092	Peptide from human

10	15	65.2	13	20	AAW86100	Peptide from human
11	15	65.2	15	23	ABG68859	CDR2 sequence remo
12	15	65.2	18	17	AA189962	Synthetic human er
13	15	65.2	19	19	AAW70915	Peptide PEP2L, hom
14	15	65.2	19	22	ABG53230	Human liver peptid
15	15	65.2	19	22	AB138408	Protein #5914 enco
16	15	65.2	19	22	AB138408	Protein #5914 enco
17	15	65.2	19	22	AAW59018	Human brain expres
18	15	65.2	19	22	AAW71548	Human bone marrow
19	15	65.2	19	22	AAW19201	Peptide #5635 enco
20	15	65.2	19	22	AAW1846	Peptide #5883 enco
21	15	65.2	19	23	ABG41359	Human peptide enco
22	15	65.2	20	19	AA121167	Human bcl2 proto-o
23	15	65.2	20	20	AA12576	Human 5' EST seque
24	15	65.2	20	22	AAW76893	Human colon cancer
25	15	65.2	21	19	AAW62904	Cytotoxic myristyl
26	15	65.2	24	20	AA13017	Human secreted pro
27	15	65.2	27	21	AAW09354	Hepatitis GB virus
28	15	65.2	27	22	ABG1645	Tyrosinase peptide
29	15	65.2	28	19	AAW48993	Lipidated vaccine
30	15	65.2	28	19	AAW48994	Lipidated vaccine
31	15	65.2	28	20	AAW09328	Lipidated vaccine
32	15	65.2	28	20	AAW09329	Lipidated vaccine
33	15	65.2	28	21	AAW12420	HCNV lipidated vac
34	15	65.2	28	21	AAW12421	HCNV lipidated vac
35	15	65.2	28	22	AAW05439	Human cytomagalovi
36	15	65.2	28	22	AAW05440	Human cytomagalovi
37	15	65.2	28	23	AAW10852	Human cytomagalovi
38	15	65.2	28	23	AAW10853	Human cytomagalovi
39	15	65.2	30	23	AAW48889	Human Tyros segmen
40	15	65.2	31	21	AAW39014	Human secreted pep
41	15	65.2	32	22	ABG57579	Human liver peptid
42	15	65.2	32	22	ABW42148	Peptide #9654 enco
43	15	65.2	32	22	ABW25710	Protein #7709 enco
44	15	65.2	32	22	AAW63033	Human brain expres
45	15	65.2	32	22	AAW75844	Human bone marrow

#### ALIGNMENTS

RESULT 1  
ABB07407  
ID ABB07407 standard; Protein; 17 AA.  
AC ABB07407;  
XX  
DT 09-APR-2002 (first entry)  
XX  
xynA fragment in plasmid pXLIN2.1.  
DE  
Xylanase; xynA; transcriptional regulation; xylan; xylose; enzyme;  
KW fungal; pharmaceutical; food; chemical.  
XX  
OS Aureobasidium pullulans.  
XX  
FN WO200196578-A2.  
XX  
PD 20-DEC-2001.  
XX  
PF 14-JUN-2001; 2001WO-US19340.  
XX  
PR 15-JUN-2000; 2000US-0595344.  
XX  
PA (UWGB-) UNIV GEORGIA RES FOUND INC.  
XX  
PI Li X, Ljungdahl LG;  
XX  
DR WPI; 2002-130735/17.  
DR N-PSDB; ABA94594.  
XX  
PT New isolated nucleic acid encoding a signal peptide for efficient and economical secreted expression of a protein of interest in a eukaryotic

PT cell, widely used in pharmaceutical, food and chemical industries -

PS Example 2; Page 29; 43pp; English.

XX

CC The invention relates to an isolated nucleic acid molecule comprising a

CC xylanase (xynA) transcriptional regulatory sequence operably linked to a

CC heterologous coding sequence. Provided is a method for producing a

CC heterologous protein in Aureobasidium pullulans, by up-regulating the

CC expression of a sequence encoding a heterologous protein by adding xylan

CC or xylose to a medium in which a recombinant A. pullulans cell comprising

CC the new isolated nucleic acid molecule is cultured, where the medium

CC contains glucose at a concentration less than 0.02 % (weight/volume) and

CC a xynA transcription regulatory sequence is operably linked to the

CC sequence encoding the heterologous protein, and the heterologous protein

CC is expressed. The nucleic acid containing a signal peptide-encoding

CC sequence, is useful for efficient and economical secreted expression of a

CC protein of interest in a eukaryotic cell, especially a fungal cell such

CC as Aureobasidium pullulans. It may be used as a probe. The proteins

CC produced are widely used in pharmaceutical, food, chemical and other

CC industries. The present sequence represents the xynA sequence around the

CC multiple cloning sites in plasmid pXLIN2.1.

XX

SQ Sequence 17 AA;

Query Match 69.6%; Score 16; DB 23; Length 17;

Best Local Similarity 25.0%; Pred. No. 3e+03;

Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8

DB 4 WSSAAALG 11

## RESULT 2

ID AAY78408 standard; peptide; 20 AA.

AC AAY78408;

DT 08-MAY-2000 (first entry)

DE Human papillomavirus E7 protein inhibiting peptide SEQ ID NO:34.

XX HPV; E7 protein; inhibition; virucide; carcinoma.

XX Human papillomavirus.

OS Synthetic.

XX EP969013-A1.

PN 05-JAN-2000.

XX 30-JUN-1998; 98EP-0112047.

PF 30-JUN-1998; 98EP-0112047.

PR (DEK-) DEUT KREBSFORSCHUNGSZENTRUM.

XX Jansen-Duerr P, Zwerschke W;

XX WPI; 2000-149116/14.

XX New peptides used for the prevention and treatment of human papilloma

PT virus associated disease -

PS Claim 1; Page 23; 26pp; English.

XX AAY78375 to AAY78415 represent peptides capable of inhibiting the human

CC papillomavirus (HPV) E7 protein. The peptides have virucide activity.

CC The peptides can be used in pharmaceutical compositions to inhibit

CC HPV E7 protein, which allows the prevention and/or treatment of HPV

CC associated diseases, which may comprise carcinomas.

XX

SQ Sequence 20 AA;

Query Match 69.6%; Score 16; DB 21; Length 20;

Best Local Similarity 25.0%; Pred. No. 3.5e+03;

Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8

DB 5 WFSASAG 12

## RESULT 3

ABB07406

ID ABB07406 standard; Protein; 20 AA.

AC ABB07406;

DT 09-APR-2002 (first entry)

DE xynA fragment in plasmid pXL2.1.

XX xylanase; xynA; transcriptional regulation; xylan; xylose; enzyme;

KW fungal; pharmaceutical; food; chemical.

XX Aureobasidium pullulans.

PN WO200196578-A2.

PD 20-DEC-2001.

PF 14-JUN-2001; 2001WO-US19340.

PR 15-JUN-2000; 2000US-0595344.

XX (UYGE-) UNIV GEORGIA RES FOUND INC.

XX Li X, Ljungdahl LG;

PI WPI; 2002-130735/17.

DR N-PSDB; ABA94593.

XX New isolated nucleic acid encoding a signal peptide for efficient and

PT economical secreted expression of a protein of interest in a eukaryotic

PT cell, widely used in pharmaceutical, food and chemical industries -

PS Example 2; Page 29; 43pp; English.

XX The invention relates to an isolated nucleic acid molecule comprising a

CC xylanase (xynA) transcriptional regulatory sequence operably linked to a

CC heterologous coding sequence. Provided is a method for producing a

CC heterologous protein in Aureobasidium pullulans, by up-regulating the

CC expression of a sequence encoding a heterologous protein by adding xylan

CC or xylose to a medium in which a recombinant A. pullulans cell comprising

CC the new isolated nucleic acid molecule is cultured, where the medium

CC contains glucose at a concentration less than 0.02 % (weight/volume) and

CC a xynA transcription regulatory sequence is operably linked to the

CC sequence encoding the heterologous protein, and the heterologous protein

CC is expressed. The nucleic acid containing a signal peptide-encoding

CC sequence, is useful for efficient and economical secreted expression of a

CC protein of interest in a eukaryotic cell, especially a fungal cell such

CC as Aureobasidium pullulans. It may be used as a probe. The proteins

CC produced are widely used in pharmaceutical, food, chemical and other

CC industries. The present sequence represents the xynA sequence around the

CC multiple cloning sites in plasmid pXL2.1.

SQ Sequence 20 AA;

Query Match 69.6%; Score 16; DB 23; Length 20;

Best Local Similarity 25.0%; Pred. No. 3.5e+03;

Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8

DB 7 WSSAAALG 14

RESULT 4  
ID AAB38243 standard; Protein; 32 AA.  
XX AAB38243;  
AC AAB38243;  
DT 30-JAN-2001 (first entry)  
DE Human secreted protein sequence encoded by gene 41 SEQ ID NO:99.  
KW Human, secreted protein; diagnosis; immunosuppressive; antiarthritic;  
KW antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;  
KW cerebroprotective; neuroprotective; antibacterial; virucide;  
KW fungicide; ophthalmological; gene therapy; autoimmune disease; infection;  
KW hyperproliferative disorder; cardiovascular disorder; angiogenesis;  
KW cerebrovascular disorder; nervous system disorder; ocular disorder;  
KW wound healing; skin aging; food additive; preservative.  
XX Homo sapiens.  
OS WO200058469-A1.  
XX PN 05-OCT-2000.  
PD 23-MAR-2000; 2000WO-US07579.  
PF 26-MAR-1999; 9SUS-0126509.  
PR 07-JAN-2000; 2000US-0174853.  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA Rosen CA, Ruben SM, Komatsoulis G;  
PI WPI, 2000-594642/56.  
DR N-PSDB; AAC69495.  
XX Isolated nucleic acid molecule encoding a human secreted protein is  
PT used in preventing, treating or ameliorating a medical condition -  
PT Claim 11; Page 375; 416pp; English.  
XX The polynucleotide sequences given in AAC69455 to AAC69502 encode the  
CC human secreted proteins given in AAB38203 to AAB38250. AAB38251 to  
CC AAB38320 represent human secreted polypeptide sequences and proteins  
CC homologous to them, which are given in the exemplification of the present  
CC invention. Human secreted proteins have activities based on the tissues  
CC and cells the genes are expressed in. Example of activities include:  
CC immunosuppressive; antiarthritic; antirheumatic; antiproliferative;  
CC cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective;  
CC neuroprotective; antibacterial; virucide; fungicide; and  
CC ophthalmological. The polynucleotides and polypeptides can be used to  
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,  
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used  
CC in diagnosing a pathological condition or susceptibility to a  
CC pathological condition. Disorders which are diagnosed or treated include  
CC autoimmune diseases, hyperproliferative disorders, cardiovascular  
CC disorders, cerebrovascular disorders, angiogenesis, nervous system  
CC disorders, infections caused by bacteria, viruses and fungi and ocular  
CC disorders. The polypeptides can also be used to aid wound healing and  
CC epithelial cell proliferation, to prevent skin aging due to sunburn, to  
CC maintain organs before transplantation, for supporting cell culture of  
CC primary tissues, to regenerate tissues and in chemotaxis. The  
CC polypeptides can also be used as a food additive or preservative to  
CC increase or decrease storage capabilities. AAC69446 to AAC69454 and  
CC AAB38202 represent sequences used in the exemplification of the present  
CC invention.  
XX SQ Sequence 32 AA;  
Query Match 69.6%; Score 16; DB 21; Length 32;

Best Local Similarity 25.0%; Pred. No. 5.1e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
DB 10 WVSATATG 17

RESULT 5  
ID AAW44053 standard; peptide; 33 AA.  
XX AAW44053;  
AC AAW44053;  
DT 26-JUN-1998 (first entry)  
DE Mutant hCS peptide.  
KW Corticostatin; somatostatin; hCS peptide; hormone-producing tumour;  
KW gastric ulcer; dementia; growth disorder; hormone secretion regulation;  
KW digestive system regulation; neural inhibitor; therapy.  
XX Synthetic.  
OS WO9746668-A1.  
XX PN 11-DEC-1997.  
PD 05-JUN-1997; 97WO-JP01911.  
PF 15-OCT-1996; 96JP-0272422.  
PR 07-JUN-1996; 96JP-0146052.  
XX 19-SEP-1996; 96JP-0247710.  
PA (TAKE ) TAKEDA CHEM IND LTD.  
PI Fukusumi S, Hinuma S, Kitada C;  
DR WPI, 1998-042177/04.  
XX N-PSDB; AAV02093.  
PT Peptide having corticostatin or somatostatin activity - useful as  
PT anticancer and antifulcer agent, and for control of dementia and  
PT growth abnormalities  
XX Disclosure; Page 117; 174pp; Japanese.  
XX This sequence is a mutant hCS peptide. It is a peptide of the  
CC invention, and has corticostatin or somatostatin activity. Antibodies  
CC recognising hCS-17 can be used to screen for a compound that modulates,  
CC i.e. an agonist or antagonist, the binding of hCS-17 to its receptor, and  
CC to assay for hCS-17, e.g. diagnosis. hCS-17, the DNA encoding it or a  
CC receptor agonist or antagonist can be used to treat and prevent  
CC hormone-producing tumours (e.g. tumours producing gastrin or insulin),  
CC gastric ulcers and dementia, regulate sleep and control growth disorders  
CC (e.g. acromegaly, gigantism and dwarfism). They can also be used to  
CC regulate hormone secretion and the digestive system (e.g. to treat  
CC diabetes), and as tumour multiplication or neural inhibitors.  
XX SQ Sequence 33 AA;  
Query Match 69.6%; Score 16; DB 19; Length 33;  
Best Local Similarity 25.0%; Pred. No. 5.2e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
DB 13 WTSQASAG 20

RESULT 6  
ID AAG94992 standard; Peptide; 10 AA.  
Query Match 69.6%; Score 16; DB 16; Length 32;



CC given species; and (c) modifying the amino acid sequence to eliminate at  
 CC least one of the T-cell epitopes identified in step (b) thereby to  
 CC eliminate or reduce the immunogenicity of the protein when exposed to the  
 CC immune system of the given species. A method of analysing a pre-existing  
 CC protein to predict the basis for immunogenic responses is also provided.  
 CC The methods can be used particularly for reducing the immunogenicity of  
 CC immunoglobulins or therapeutic proteins, e.g. Streptokinase. The  
 CC products can be used for diagnosis and therapy. Sequences AAW86075-W86114  
 CC represent peptides from humanised A33 heavy chain variable region  
 CC predicted by peptide threading.

XX Sequence 13 AA;

Query Match 65.2%; Score 15; DB 20; Length 13;

Best Local Similarity 25.0%; Pred. No. 4.1e+03;

Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8

DB 5 WVATISSG 12

RESULT 9

AAW86092  
 ID AAW86092 standard; peptide; 13 AA.

XX AAW86092;

DT 03-MAR-1999 (first entry)

DE Peptide from humanised A33 heavy chain variable region.

KW Non-immunogenic; epitope; T-cell; immunogenicity; immune system;  
 immunoglobulin; therapeutic; streptokinase; diagnosis; human; A33.

XX Homo sapiens.

XX WO9852976-A1.

XX 26-NOV-1998.

XX 21-MAY-1998; 98WO-GB01473.

XX 14-APR-1998; 98GB-0007751.

XX 21-MAY-1997; 97GB-0010480.

XX 31-JUL-1997; 97GB-0016197.

XX 28-NOV-1997; 97GB-0025270.

XX 02-DEC-1997; 97US-0067235.

XX (BIOV-) BIOVATION LTD.

XX Carr FU;

XX WPI; 1999-045301/04.

XX Reducing immunogenicity of proteins - by modifying the amino acid  
 PT sequence of the protein to eliminate potential epitopes for T-cells  
 PT of a given species

XX Example 5; Page 33; 77pp; English.

XX The invention relates to a method for the production of non-immunogenic  
 CC proteins. The method comprises determining at least part of the amino  
 CC acid sequence of the protein; (b) identifying in the amino acid sequence  
 CC one or more potential epitopes for T-cells (T-cell epitopes) of the  
 CC given species; and (c) modifying the amino acid sequence to eliminate at  
 CC least one of the T-cell epitopes identified in step (b) thereby to  
 CC eliminate or reduce the immunogenicity of the protein when exposed to the  
 CC immune system of the given species. A method of analysing a pre-existing  
 CC protein to predict the basis for immunogenic responses is also provided.  
 CC The methods can be used particularly for reducing the immunogenicity of  
 CC immunoglobulins or therapeutic proteins, e.g. Streptokinase. The  
 CC products can be used for diagnosis and therapy. Sequences AAW86075-W86114

CC represent peptides from humanised A33 heavy chain variable region  
 CC predicted by peptide threading.

XX Sequence 13 AA;

Query Match 65.2%; Score 15; DB 20; Length 13;

Best Local Similarity 25.0%; Pred. No. 4.1e+03;

Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8

DB 2 WVATISSG 9

RESULT 10

AAW86100

ID AAW86100 standard; peptide; 13 AA.

XX AAW86100;

DT 03-MAR-1999 (first entry)

DE Peptide from humanised A33 heavy chain variable region.

KW Non-immunogenic; epitope; T-cell; immunogenicity; immune system;  
 immunoglobulin; therapeutic; streptokinase; diagnosis; human; A33.

XX Homo sapiens.

XX WO9852976-A1.

XX 26-NOV-1998.

XX 21-MAY-1998; 98WO-GB01473.

XX 14-APR-1998; 98GB-0007751.

XX 21-MAY-1997; 97GB-0010480.

XX 31-JUL-1997; 97GB-0016197.

XX 28-NOV-1997; 97GB-0025270.

XX 02-DEC-1997; 97US-0067235.

XX (BIOV-) BIOVATION LTD.

XX Carr FU;

XX WPI; 1999-045301/04.

XX Reducing immunogenicity of proteins - by modifying the amino acid  
 PT sequence of the protein to eliminate potential epitopes for T-cells  
 PT of a given species

XX Example 5; Page 34; 77pp; English.

XX The invention relates to a method for the production of non-immunogenic  
 CC proteins. The method comprises determining at least part of the amino  
 CC acid sequence of the protein; (b) identifying in the amino acid sequence  
 CC one or more potential epitopes for T-cells (T-cell epitopes) of the  
 CC given species; and (c) modifying the amino acid sequence to eliminate at  
 CC least one of the T-cell epitopes identified in step (b) thereby to  
 CC eliminate or reduce the immunogenicity of the protein when exposed to the  
 CC immune system of the given species. A method of analysing a pre-existing  
 CC protein to predict the basis for immunogenic responses is also provided.  
 CC The methods can be used particularly for reducing the immunogenicity of  
 CC immunoglobulins or therapeutic proteins, e.g. Streptokinase. The  
 CC products can be used for diagnosis and therapy. Sequences AAW86075-W86114  
 CC represent peptides from humanised A33 heavy chain variable region  
 CC predicted by peptide threading.

XX Sequence 13 AA;

Query Match 65.2%; Score 15; DB 20; Length 13;

Best Local Similarity 25.0%; Pred. No. 4.1e+03;

Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
 2 WATISSG 9

Db

RESULT 11  
 ABG68859  
 ID ABG68859 standard; Peptide; 15 AA.  
 XX AC  
 XX ABG68859;  
 DT 07-OCT-2002 (first entry)  
 DE CDR2 sequence removed from cIFNcFv construct.  
 XX  
 KW Cytostatic; virucide; hepatotropic; antiinflammatory; neuroprotective;  
 KW immunosuppressive; antiarthritic; cytokine receptor; interferon; IFN;  
 KW cancer; haematological malignancy; viral infection; hepatitis; human;  
 KW multiple sclerosis; autoimmune disease; arthritis.  
 XX  
 OS Synthetic.  
 XX WO200244197-A2.  
 PN 06-JUN-2002.  
 XX  
 PD 30-NOV-2001; 2001WO-CA01701.  
 PF 01-DEC-2000; 2000US-0727388.  
 PR (FISH/) FISH E N.  
 PA Fish EN;  
 XX WPI; 2002-547689/58.  
 DR N-PSDB; ABK97822.  
 XX Cytokine receptor binding peptide construct, in particular interferon  
 PT receptor binding peptide construct for use as an interferon mimetic,  
 PT comprises a cytokine receptor binding domain incorporated in a  
 PT molecular scaffold -  
 XX Example 8; Page 51; 105pp; English.

CC This invention relates to a novel cytokine receptor binding peptide  
 CC construct comprising a cytokine receptor binding domain incorporated in  
 CC a suitable molecular scaffold so that the scaffold maintains the binding  
 CC domain in a configuration suitable for binding to the cytokine receptor.  
 CC The peptides of the invention may have cytostatic, virucide,  
 CC hepatotropic, antiinflammatory, neuroprotective, immunosuppressive and  
 CC antiarthritic activities. A new interferon receptor binding peptide  
 CC construct is useful in the manufacture of a medicament as an interferon  
 CC (IFN) mimetic. A peptide that mimics the effect of IFN is useful in  
 CC medical therapies for cancer, haematological malignancies, viral  
 CC infections (hepatitis B or C), multiple sclerosis and autoimmune  
 CC diseases such as arthritis, to detect modulators of IFN action, in  
 CC screening assays to compare the activity and/or interaction with  
 CC another molecule or potential IFN modulator and also in the diagnosis  
 CC of IFN activity related disorders. A nucleic acid encoding the  
 CC peptide of the invention or is useful for the treatment and therapy of  
 CC the mentioned medical conditions. The peptide of the invention has less  
 CC side effect than those of native cytokines. The present sequence  
 CC represents an interferon receptor binding peptide of the invention.

XX  
 SQ Sequence 15 AA;  
 Query Match 65.2%; Score 15; DB 23; Length 15;  
 Best Local Similarity 25.0%; Pred. No. 4.7e+03;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
 2 WATISSG 9

Db

RESULT 12  
 AAR89962  
 ID AAR89962 standard; peptide; 18 AA.  
 XX AC  
 XX AAR89962;  
 DT 28-SEP-1996 (first entry)  
 DE Synthetic human erythropoietin receptor peptide, SE-2B.  
 XX  
 KW Monoclonal antibody; erythropoietin receptor; diagnosis; anaemia;  
 KW erythropoiesis; erythrocyte production; epitope mapping.  
 XX  
 OS Synthetic.  
 XX WO9603438-A1.  
 PN 08-FEB-1996.  
 PD 26-JUL-1995; 95WO-US09458.  
 PF 26-JUL-1994; 94US-0280864.  
 PR (AMGE-) AMGEN INC.  
 PA Elliott SG;  
 PI WPI; 1996-117004/12.  
 DR Monoclonal antibodies stimulating an erythropoietin receptor -  
 PT useful in diagnosis and treatment of patients having disorders  
 PT associated with low red blood cell levels, e.g. anaemia  
 XX Example 6; Page 34; 61pp; English.

CC AAR89960-R89965 and AAR89936-R89939 are overlapping, synthetic human  
 CC erythropoietin receptor (shuEPOR) peptides which span residues 1 to  
 CC 244 of the human EPOR. The peptides are used to map the EPOR binding  
 CC epitope of an EPOR monoclonal antibody which binds to EPORs and  
 CC stimulates erythropoiesis by stimulating the proliferation and/or  
 CC differentiation of erythroid progenitor cells to erythrocytes.  
 CC Pharmaceutical compans. contg. the antibody may be used in the  
 CC diagnosis and treatment of patients having disorders associated with  
 CC low red blood cell levels, e.g. anaemia. The antibodies are also  
 CC useful in methods and kits for detecting EPORs in biological in  
 CC biological samples.

XX  
 SQ Sequence 18 AA;  
 Query Match 65.2%; Score 15; DB 17; Length 18;  
 Best Local Similarity 25.0%; Pred. No. 5.4e+03;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
 3 WEERASAG 10

Db

RESULT 13  
 AAW70915  
 ID AAW70915 standard; peptide; 19 AA.  
 XX AC  
 XX AAW70915;  
 DT 14-OCT-1998 (first entry)  
 DE Peptide PEP2L, homologous to light chain CDR2 of antibody RS-348.  
 XX Pathogenic virus; tropism; mucosa; CDR region; monoclonal antibody;  
 KW respiratory syncytial virus; RSV; VP6 protein; rota virus; RV;

KW viral infection; inhibit; fusion; protection; transcription; translation;  
 KW antiviral agent; prophylaxis; diagnosis; infection; contamination.

OS Synthetic.  
 OS Mus sp.

PN FR2758331-A1.

XX 17-JUL-1998.

XX 14-JAN-1997; 97FR-0000300.

XX 14-JAN-1997; 97FR-0000300.

XX (UYBO-) UNIV BOURGOGNE.

XX Bourgeois C, Kohli E, Pothier P;

XX WPI; 1998-390320/34.

XX New peptide(s) recognising viral epitope with tropism to mucosa -  
 PT useful for, e.g. diagnosing, preventing and treating viral  
 PT infection(s)

PS Claim 8; Fig 5; 5lpp; French.

CC AAW70905-46 represent peptide sequences that can recognise, by  
 CC antigen-antibody type reactions, at least 1 epitope of a pathogenic  
 CC virus having tropism for the mucosa. AAW70905-16 and AAW70929-46 are  
 CC analogous to CDR regions of monoclonal antibodies specific for  
 CC respiratory syncytial virus (RSV). AAW70917-28 are analogous to CDR  
 CC regions of monoclonal antibodies specific for site III or IV of the  
 CC VP6 protein of rota virus (RV). The peptides can neutralise viral  
 CC infections and may also inhibit fusion between infected and uninfected  
 CC cells or cells and viruses. They provide passive or active protection  
 CC and/or inhibit transcription of the virus, so are useful as antiviral  
 CC agents or for prophylaxis, in human or veterinary medicine. The peptides  
 CC can be labelled and used to diagnose infection or contamination by the  
 CC virus. The peptides are particularly directed against RSV or RS but may  
 CC also be used against papilloma, adeno, entero, polio, influenza or  
 CC immune deficiency viruses.

XX Sequence 19 AA;

Query Match 65.2%; Score 15; DB 19; Length 19;  
 Best Local Similarity 25.0%; Pred. No. 5.6e+03;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 WXXXXXXG 8  
 Db 7 WASTRDSG 14

RESULT 14

ABG53230

ID ABG53230 standard; Peptide; 19 AA.

XX AC ABG53230;

XX 25-FEB-2003 (first entry)

XX Human liver peptide, SEQ ID No 31878.

XX Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;  
 XX hypercholesterolaemia; coronary heart disease.

XX Homo sapiens.

XX WO200157273-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00664.

XX

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488898/53.

XX Human genome-derived single exon nucleic acid probes useful for  
 PT analysing gene expression in human adult liver -

XX Claim 27; SEQ ID No 31878; 659pp; English.

XX The invention relates to a single exon nucleic acid probe (SEN) (I) for  
 CC measuring human gene expression in a sample derived from human adult  
 CC liver comprising one of 13109 defined nucleotide sequences given in the  
 CC specification (or complements/ fragments). The probe hybridises at high  
 CC stringency to a nucleic acid molecule expressed in the human adult  
 CC liver. (I) may be used for predicting, measuring and displaying gene  
 CC expression in samples derived from human adult liver. The genes  
 CC identified may be involved in genetic liver diseases such as cirrhosis,  
 CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which  
 CC is associated with coronary heart disease. ABG47348-ABG59930 represent  
 CC human liver single exon encoded peptides of the invention.  
 CC Note: The sequence information for this patent does not appear in the  
 CC printed specification but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 19 AA;

Query Match 65.2%; Score 15; DB 22; Length 19;  
 Best Local Similarity 25.0%; Pred. No. 5.6e+03;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 WXXXXXXG 8  
 Db 3 WGRSSTTG 10

RESULT 15

ABB38408

ID ABB38408 standard; Peptide; 19 AA.

XX AC ABB38408;

XX 04-FEB-2002 (first entry)

XX Peptide #5914 encoded by human foetal liver single exon probe.

XX Human; foetal liver; gene expression; single exon nucleic acid probe.

XX Homo sapiens.

XX WO200157277-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00669.

XX 04-FEB-2000; 2000US-0180312.

XX 26-MAY-2000; 2000US-0207456.

XX 30-JUN-2000; 2000US-0608408.

XX 03-AUG-2000; 2000US-0632366.

XX 21-SEP-2000; 2000US-0234687.

XX 27-SEP-2000; 2000US-0236359.

XX 04-OCT-2000; 2000GB-0024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX DR WPI; 2001-483447/52.  
 XX PT Human genome-derived single exon nucleic acid probes useful for  
 XX PT analyzing gene expression in human fetal liver -  
 XX PS Claim 27; SEQ ID NO 31043; 639pp. + sequence listing; English.  
 XX CC The invention relates to a single exon nucleic acid probe for  
 CC measuring human gene expression in a sample derived from human foetal  
 CC liver. The single exon nucleic acid probes may be used for predicting,  
 CC measuring and displaying gene expression in samples derived from human  
 CC fetal liver. The present sequence is a peptide encoded by a single exon  
 CC nucleic acid probe of the invention.  
 CC Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX SQ Sequence 19 AA;  
 Query Match 65.2%; Score 15; DB 22; Length 19;  
 Best Local Similarity 25.0%; Pred. No. 5.6e+03;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 WXXXXXXG 8  
 Db 3 WRRSSTTG 10

Search completed: January 12, 2004, 10:05:04  
 Job time : 42 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 12, 2004, 08:11:07 ; Search time 70 Seconds

(without alignments)

23.030 Million cell updates/sec

Title: US-09-185-908-1

Perfect score: 23

Sequence: 1 WXXXXXXG 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747907 seqs, 201509753 residues

Total number of hits satisfying chosen parameters: 226452

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

```
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	69.6	50	11	US-09-948-783-125
2	15	65.2	10	11	US-09-572-404B-1186
3	15	65.2	10	11	US-09-572-404B-1186
4	15	65.2	13	12	US-10-300-215-60
5	15	65.2	13	12	US-10-300-215-68
6	15	65.2	13	12	US-10-300-215-73
7	15	65.2	18	12	US-10-364-276-6
8	15	65.2	19	9	US-09-864-761-38884
9	15	65.2	20	12	US-10-280-066-61
10	15	65.2	20	12	US-10-280-066-94
11	15	65.2	20	15	US-10-106-698-7667
12	15	65.2	22	12	US-10-307-724-127
13	15	65.2	22	12	US-10-307-724-129
14	15	65.2	27	8	US-08-424-550B-481
15	15	65.2	28	12	US-10-405-231-35

16	15	65.2	28	12	US-10-405-231-36	Sequence 36, Appl
17	15	65.2	28	15	US-10-238-607-35	Sequence 35, Appl
18	15	65.2	28	15	US-10-238-607-36	Sequence 36, Appl
19	15	65.2	31	12	US-09-962-756-1276	Sequence 1276, Ap
20	15	65.2	31	12	US-10-253-471-1276	Sequence 1276, Ap
21	15	65.2	32	9	US-09-864-761-41008	Sequence 41008, A
22	15	65.2	34	11	US-09-764-891-4811	Sequence 4811, Ap
23	15	65.2	34	15	US-10-091-572-366	Sequence 366, App
24	15	65.2	36	11	US-09-883-343A-69	Sequence 69, Appl
25	15	65.2	36	12	US-09-962-756-1310	Sequence 1310, Ap
26	15	65.2	36	12	US-10-253-471-1310	Sequence 1310, Ap
27	15	65.2	37	9	US-09-864-761-40556	Sequence 40556, A
28	15	65.2	37	15	US-10-007-521-64	Sequence 64, Appl
29	15	65.2	39	9	US-09-864-761-48977	Sequence 48977, A
30	15	65.2	39	12	US-10-029-386-33891	Sequence 33891, A
31	15	65.2	40	12	US-10-029-386-33430	Sequence 3430, A
32	15	65.2	43	12	US-09-880-573-57	Sequence 57, Appl
33	15	65.2	44	9	US-09-864-761-34910	Sequence 34910, A
34	15	65.2	44	9	US-09-864-761-37541	Sequence 37541, A
35	15	65.2	44	9	US-09-864-761-40294	Sequence 40294, A
36	15	65.2	44	9	US-09-864-761-44325	Sequence 44325, A
37	15	65.2	46	15	US-10-106-698-7164	Sequence 7164, Ap
38	15	65.2	46	15	US-10-106-698-7164	Sequence 7164, Ap
39	15	65.2	47	10	US-09-764-877-1793	Sequence 1793, Ap
40	15	65.2	49	9	US-09-864-761-41134	Sequence 41134, A
41	15	65.2	50	9	US-09-864-761-46317	Sequence 46317, A
42	14	60.9	8	10	US-09-185-908-42	Sequence 42, Appl
43	14	60.9	8	10	US-09-185-908-163	Sequence 163, App
44	14	60.9	9	10	US-09-835-948-72	Sequence 72, Appl
45	14	60.9	9	12	US-10-172-597-72	Sequence 72, Appl

#### ALIGNMENTS

```
RESULT 1
US-09-948-783-125
; Sequence 125, Application US/09948783
; Publication No. US20030100051A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et. al.
; TITLE OF INVENTION: 97 Human secreted proteins
; FILE REFERENCE: P2028P2
; CURRENT APPLICATION NUMBER: US/09/948,783
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231,846
; PRIOR FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: 09/892,877
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: 09/437,658
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: PCT/US99/09847
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: 60/085,093
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/085,094
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/085,105
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/085,180
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/085,927
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,906
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,924
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,922
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,921
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,923
; PRIOR FILING DATE: 1998-05-18
```

us-09-185-908-1.slim50.rapb

Mon Jan 12 08:42:31 2004

PRIOR APPLICATION NUMBER: 60/085,925  
PRIOR FILING DATE: 1998-05-18  
BEST LOCAL SIMILARITY: 60/085,928  
PRIOR FILING DATE: 1998-05-18  
PRIOR APPLICATION NUMBER: 60/085,920  
PRIOR FILING DATE: 1998-05-18  
NUMBER OF SEQ ID NOS: 465  
SOFTWARE: Patentin ver. 2.0  
SEQ ID NO 125  
LENGTH: 50  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-948-783-125

Query Match 69.6%; Score 15; DB 11; Length 50;  
Best Local Similarity 25.0%; Pred. No. 9.3e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
DB 34 WTSSMATG 41

RESULT 2  
US-09-572-404B-1186  
Sequence 1186, Application US/09572404B  
Publication No. US20030078374A1  
GENERAL INFORMATION:  
APPLICANT: Proteom Ltd  
TITLE OF INVENTION: Complementary peptide ligands from the human genome  
FILE REFERENCE: Human patent  
CURRENT APPLICATION NUMBER: US/09/572,404B  
CURRENT FILING DATE: 2000-05-17  
NUMBER OF SEQ ID NOS: 4203  
SOFTWARE: ProtPatent version 1.0  
SEQ ID NO 1186  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo Sapiens  
FEATURE:  
OTHER INFORMATION: sequence located in TMPO at 231-240 and may interact with Sequenc  
US-09-572-404B-1186

Query Match 65.2%; Score 15; DB 11; Length 10;  
Best Local Similarity 25.0%; Pred. No. 5.6e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
DB 2 WTSGSSKG 9

RESULT 3  
US-09-572-404B-1188  
Sequence 1188, Application US/09572404B  
Publication No. US20030078374A1  
GENERAL INFORMATION:  
APPLICANT: Proteom Ltd  
TITLE OF INVENTION: Complementary peptide ligands from the human genome  
FILE REFERENCE: Human patent  
CURRENT APPLICATION NUMBER: US/09/572,404B  
CURRENT FILING DATE: 2000-05-17  
NUMBER OF SEQ ID NOS: 4203  
SOFTWARE: ProtPatent version 1.0  
SEQ ID NO 1188  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo Sapiens  
FEATURE:  
OTHER INFORMATION: sequence located in TMPO at 230-239 and may interact with Sequenc  
US-09-572-404B-1188

Query Match 65.2%; Score 15; DB 11; Length 10;  
Best Local Similarity 25.0%; Pred. No. 5.6e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
DB 2 WTSGSSKG 10

RESULT 4  
US-10-300-215-60  
Sequence 60, Application US/10300215  
Publication No. US20030153043A1  
GENERAL INFORMATION:  
APPLICANT: CARR, Francis Joseph  
APPLICANT: ADAIR, Fiona Suzanne  
APPLICANT: HAMILTON, Anita Anne  
APPLICANT: CARTER, Graham  
TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF  
TITLE OF INVENTION: NON-IMMUNOGENIC PROTEINS  
FILE REFERENCE: MER-104-CON.1  
CURRENT APPLICATION NUMBER: US/10/300,215  
CURRENT FILING DATE: 2002-11-20  
PRIOR APPLICATION NUMBER: US 09/438,136  
PRIOR FILING DATE: 1999-11-10  
PRIOR APPLICATION NUMBER: WO PCT/GB98/01473  
PRIOR FILING DATE: 1998-05-21  
PRIOR APPLICATION NUMBER: GB 9710480.6  
PRIOR FILING DATE: 1997-05-21  
PRIOR APPLICATION NUMBER: GB 9716197.0  
PRIOR FILING DATE: 1997-07-31  
PRIOR APPLICATION NUMBER: GB 9725270.4  
PRIOR FILING DATE: 1997-11-28  
PRIOR APPLICATION NUMBER: GB 9807751.4  
PRIOR FILING DATE: 1998-04-14  
PRIOR APPLICATION NUMBER: US 60/067,235  
PRIOR FILING DATE: 1997-12-02  
NUMBER OF SEQ ID NOS: 254  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 60  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: humanized monoclonal antibody fragments  
US-10-300-215-60

Query Match 65.2%; Score 15; DB 12; Length 13;  
Best Local Similarity 25.0%; Pred. No. 6.6e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
DB 2 WWTATISSG 9

RESULT 5  
US-10-300-215-68  
Sequence 68, Application US/10300215  
Publication No. US20030153043A1  
GENERAL INFORMATION:  
APPLICANT: CARR, Francis Joseph  
APPLICANT: ADAIR, Fiona Suzanne  
APPLICANT: HAMILTON, Anita Anne  
APPLICANT: CARTER, Graham  
TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF  
TITLE OF INVENTION: NON-IMMUNOGENIC PROTEINS  
FILE REFERENCE: MER-104-CON.1  
CURRENT APPLICATION NUMBER: US/10/300,215  
CURRENT FILING DATE: 2002-11-20  
PRIOR APPLICATION NUMBER: US 09/438,136  
PRIOR FILING DATE: 1999-11-10

PRIOR APPLICATION NUMBER: WO PCT/GB98/01473  
PRIOR FILING DATE: 1998-05-21  
PRIOR APPLICATION NUMBER: GB 9710480.6  
PRIOR FILING DATE: 1997-05-21  
PRIOR APPLICATION NUMBER: GB 9716197.0  
PRIOR FILING DATE: 1997-07-31  
PRIOR APPLICATION NUMBER: GB 9725270.4  
PRIOR FILING DATE: 1997-11-28  
PRIOR APPLICATION NUMBER: GB 9807751.4  
PRIOR FILING DATE: 1998-04-14  
PRIOR APPLICATION NUMBER: US 60/067,235  
PRIOR FILING DATE: 1997-12-02  
NUMBER OF SEQ ID NOS: 254  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 68  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: humanized monoclonal antibody fragments  
US-10-300-215-68

Query Match 65.2%; Score 15; DB 12; Length 13;  
Best Local Similarity 25.0%; Pred. No. 6.6e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
Db 2 WVATISSG 9

RESULT 6  
US-10-300-215-73  
Sequence 73, Application US/10300215  
Publication No. US20030153043A1  
GENERAL INFORMATION:  
APPLICANT: CARR, Francis Joseph  
APPLICANT: ADAIR, Fiona Suzanne  
APPLICANT: HAMILTON, Anita Anne  
APPLICANT: CARTER, Graham  
TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF  
TITLE OF INVENTION: NON-IMMUNOGENIC PROTEINS  
FILE REFERENCE: MER-104-Con.1  
CURRENT APPLICATION NUMBER: US/10/300,215  
PRIOR FILING DATE: 2002-11-20  
PRIOR APPLICATION NUMBER: US 09/438,136  
PRIOR FILING DATE: 1999-11-10  
PRIOR APPLICATION NUMBER: WO PCT/GB98/01473  
PRIOR FILING DATE: 1998-05-21  
PRIOR APPLICATION NUMBER: GB 9710480.6  
PRIOR FILING DATE: 1997-05-21  
PRIOR APPLICATION NUMBER: GB 9716197.0  
PRIOR FILING DATE: 1997-07-31  
PRIOR APPLICATION NUMBER: GB 9725270.4  
PRIOR FILING DATE: 1997-11-28  
PRIOR APPLICATION NUMBER: GB 9807751.4  
PRIOR FILING DATE: 1998-04-14  
PRIOR APPLICATION NUMBER: US 60/067,235  
PRIOR FILING DATE: 1997-12-02  
NUMBER OF SEQ ID NOS: 254  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 73  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: humanized monoclonal antibody fragments  
US-10-300-215-73

Query Match 65.2%; Score 15; DB 12; Length 13;  
Best Local Similarity 25.0%; Pred. No. 6.6e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
Db 5 WVATISSG 12

RESULT 7  
US-10-364-276-6  
Sequence 6, Application US/10364276  
Publication No. US20030215444A1  
GENERAL INFORMATION:  
APPLICANT: Elliott, Steven G  
TITLE OF INVENTION: Antibodies which Activate an Erythropoietin Receptor  
FILE REFERENCE: 06843-0030-04000  
CURRENT APPLICATION NUMBER: US/10/364,276  
CURRENT FILING DATE: 2003-06-17  
PRIOR APPLICATION NUMBER: 09/092,671  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 08/280,864  
PRIOR FILING DATE: 1994-07-26  
PRIOR APPLICATION NUMBER: 09/640,090  
PRIOR FILING DATE: 2000-08-17  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-10-364-276-6

Query Match 65.2%; Score 15; DB 12; Length 18;  
Best Local Similarity 25.0%; Pred. No. 8e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
Db 3 WEEAASAG 10

RESULT 8  
US-09-864-761-38884  
Sequence 38884, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharron G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
FILE REFERENCE: Aeonica-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 38884  
LENGTH: 19  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC004624.6  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.9  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.5  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1  
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.1  
US-09-864-761-38884

Query Match 65.2%; Score 15; DB 9; Length 19;  
Best Local Similarity 25.0%; Pred. No. 8.3e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
Db 3 WKRSSTG 10

RESULT 9  
US-10-280-066-61  
Sequence 61, Application US/10280066  
Publication No. US20030180718A1  
GENERAL INFORMATION:  
APPLICANT: Pillutla, Renuka C.  
APPLICANT: Brissette, Renee  
APPLICANT: Spruyt, Michael  
APPLICANT: Dedova, Olga  
APPLICANT: Blume, Arthur J.  
APPLICANT: Prendergast, John  
APPLICANT: Goldstein, Neil I.  
TITLE OF INVENTION: TARGET SPECIFIC SCREENING AND ITS USE FOR IDENTIFYING TARGET BIND  
FILE REFERENCE: 2598-4009US1  
CURRENT APPLICATION NUMBER: US/10/280,066  
CURRENT FILING DATE: 2002-10-24  
PRIOR APPLICATION NUMBER: 60/345,471  
PRIOR FILING DATE: 2001-10-24  
NUMBER OF SEQ ID NOS: 537  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 61  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Escherichia coli  
FEATURE:  
NAME/KEY: MISC FEATURE  
OTHER INFORMATION: DGI-2-20F-PP-E7  
US-10-280-066-61

Query Match 65.2%; Score 15; DB 12; Length 20;  
Best Local Similarity 25.0%; Pred. No. 8.5e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
Db 10 WTASRTGG 17

RESULT 10  
US-10-280-066-94  
Sequence 94, Application US/10280066  
Publication No. US20030180718A1  
GENERAL INFORMATION:  
APPLICANT: Pillutla, Renuka C.  
APPLICANT: Brissette, Renee  
APPLICANT: Spruyt, Michael  
APPLICANT: Dedova, Olga  
APPLICANT: Blume, Arthur J.  
APPLICANT: Prendergast, John  
APPLICANT: Goldstein, Neil I.  
TITLE OF INVENTION: TARGET SPECIFIC SCREENING AND ITS USE FOR IDENTIFYING TARGET BI  
FILE REFERENCE: 2598-4009US1  
CURRENT APPLICATION NUMBER: US/10/280,066  
CURRENT FILING DATE: 2002-10-24  
PRIOR APPLICATION NUMBER: 60/345,471  
PRIOR FILING DATE: 2001-10-24  
NUMBER OF SEQ ID NOS: 537  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 94  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Escherichia coli  
FEATURE:  
NAME/KEY: MISC FEATURE  
OTHER INFORMATION: DGI-2-20R-3-D9  
US-10-280-066-94

Query Match 65.2%; Score 15; DB 12; Length 20;  
Best Local Similarity 25.0%; Pred. No. 8.5e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
Db 8 WASGSGAG 15

RESULT 11  
US-10-106-698-7667  
Sequence 7667, Application US/10106698  
Publication No. US20030109690A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept  
FILE REFERENCE: PA005P1  
CURRENT APPLICATION NUMBER: US/10/106,698  
CURRENT FILING DATE: 2002-03-27  
PRIOR APPLICATION NUMBER: PCT/US00/36524  
PRIOR FILING DATE: 2000-09-28  
PRIOR APPLICATION NUMBER: US 60/157,137  
PRIOR FILING DATE: 1999-09-29  
PRIOR APPLICATION NUMBER: US 60/163,280  
PRIOR FILING DATE: 1999-11-03  
NUMBER OF SEQ ID NOS: 8564  
SOFTWARE: PatentIn Ver. 3.0  
SEQ ID NO 7667  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: MISC FEATURE  
LOCATION: (16)  
US-10-106-698-7667

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
NAME/KEY: MISC FEATURE  
LOCATION: (19)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-10-106-698-7667

Query Match 65.2%; Score 15; DB 15; Length 20;  
Best Local Similarity 25.0%; Pred. No. 8.5e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
Db 4 WAAQSSG 11

## RESULT 12

US-10-307-724-127  
Sequence 127, Application US/10307724  
Publication No. US20030232972A1  
GENERAL INFORMATION:  
APPLICANT: Bowdish, Katherine S.  
APPLICANT: Frederickson, Shana  
APPLICANT: Renshaw, Mark  
TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES  
FILE REFERENCE: 1087-2c1p  
CURRENT APPLICATION NUMBER: US/10/307,724  
CURRENT FILING DATE: 2002-12-02  
PRIOR APPLICATION NUMBER: US 60/251,448  
PRIOR FILING DATE: 2000-12-05  
PRIOR APPLICATION NUMBER: US 60/288,889  
PRIOR FILING DATE: 2001-05-04  
PRIOR APPLICATION NUMBER: US 60/294,068  
PRIOR FILING DATE: 2001-05-29  
PRIOR APPLICATION NUMBER: US 10/006,593  
PRIOR FILING DATE: 2001-12-05  
NUMBER OF SEQ ID NOS: 134  
SOFTWARE: Patent in version 3.2  
SEQ ID NO 127  
LENGTH: 22  
TYPE: PRT  
ORGANISM: artificial sequence  
FEATURE:  
OTHER INFORMATION: heavy chain CDR2 clone  
US-10-307-724-127

Query Match 65.2%; Score 15; DB 12; Length 22;  
Best Local Similarity 25.0%; Pred. No. 9.1e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
Db 14 WLAARAAG 21

## RESULT 13

US-10-307-724-129  
Sequence 129, Application US/10307724  
Publication No. US20030232972A1  
GENERAL INFORMATION:  
APPLICANT: Bowdish, Katherine S.  
APPLICANT: Frederickson, Shana  
APPLICANT: Renshaw, Mark  
TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES  
FILE REFERENCE: 1087-2c1p  
CURRENT APPLICATION NUMBER: US/10/307,724  
CURRENT FILING DATE: 2002-12-02  
PRIOR APPLICATION NUMBER: US 60/251,448  
PRIOR FILING DATE: 2000-12-05  
PRIOR APPLICATION NUMBER: US 60/288,889  
PRIOR FILING DATE: 2001-05-04  
PRIOR APPLICATION NUMBER: US 60/294,068  
PRIOR FILING DATE: 2001-05-29  
PRIOR APPLICATION NUMBER: US 10/006,593

PRIOR FILING DATE: 2001-12-05  
NUMBER OF SEQ ID NOS: 134  
SOFTWARE: Patent in version 3.2  
SEQ ID NO 129  
LENGTH: 22  
TYPE: PRT  
ORGANISM: artificial sequence  
FEATURE:  
OTHER INFORMATION: heavy chain CDR2 clone  
US-10-307-724-129

Query Match 65.2%; Score 15; DB 12; Length 22;  
Best Local Similarity 25.0%; Pred. No. 9.1e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
Db 14 WLAARATG 21

## RESULT 14

US-08-424-550B-481  
Sequence 481, Application US/08424550B  
Publication No. US20020119447A1  
GENERAL INFORMATION:  
APPLICANT: JOHN N. SIMONS  
APPLICANT: TAMI J. PILOT-MATIAS  
APPLICANT: GEORGE J. DAWSON  
APPLICANT: GEORGE G. SCHLAUDER  
APPLICANT: SURESH M. DESAI  
APPLICANT: THOMAS P. LEARY  
APPLICANT: ANTHONY SCOTT MUERHOFF  
APPLICANT: JAMES C. ERKER  
APPLICANT: SHERI L. BUIJK  
APPLICANT: ISA K. MUSHAWAR  
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE  
NUMBER OF SEQUENCES: 716  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
STREET: 100 ABBOTT PARK ROAD  
CITY: ABBOTT PARK  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/424,550B  
FILING DATE:  
CLASSIFICATION: 435435  
ATTORNEY/AGENT INFORMATION:  
NAME: FOREMSKI, PRISCILLA E.  
REGISTRATION NUMBER: 33,207  
REFERENCE/DOCKET NUMBER: 5527.PC.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 708-937-6365  
TELEFAX: 708-938-2623  
INFORMATION FOR SEQ ID NO: 481:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-424-550B-481

Query Match 65.2%; Score 15; DB 8; Length 27;  
Best Local Similarity 25.0%; Pred. No. 1e+04;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
Db 14 WLAARAAG 21

QY 1 WXXXXXXG 8  
DB 14 WTRSSALG 21

RESULT 15  
US-10-405-231-35  
; Sequence 35, Application US/10405231  
; Publication No. US20030190328A1  
; GENERAL INFORMATION:  
; APPLICANT: Diamond, Don J.  
; TITLE OF INVENTION: IMMUNO-REACTIVE PEPTIDE CTL EPITOPES OF HUMAN CYTOMEGALOVIRUS  
; FILE REFERENCE: 1954-346  
; CURRENT APPLICATION NUMBER: US/10/405,231  
; CURRENT FILING DATE: 2003-04-03  
; PRIOR APPLICATION NUMBER: US/09/692,170C  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: US 09/534,639  
; PRIOR FILING DATE: 2000-03-27  
; PRIOR APPLICATION NUMBER: US 09/075,257  
; PRIOR FILING DATE: 1998-05-11  
; PRIOR APPLICATION NUMBER: US 09/021,298  
; PRIOR FILING DATE: 1998-02-10  
; PRIOR APPLICATION NUMBER: US 08/950,064  
; PRIOR FILING DATE: 1997-10-14  
; PRIOR APPLICATION NUMBER: US 08/747,488  
; PRIOR FILING DATE: 1996-11-12  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 35  
; LENGTH: 28  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct for human cytomegalovirus vaccine  
; FEATURE:  
; NAME/KEY: LIPID  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: DIPALMITATE  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (6)..(6)  
; OTHER INFORMATION: Xaa = F or cyclohexylalanine  
US-10-405-231-35

Query Match 65.2%; Score 15; DB 12; Length 28;  
Best Local Similarity 25.0%; Pred. No. 1.1e+04;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
DB 10 WTLKAAAG 17

Search completed: January 12, 2004, 08:21:32  
Job time : 73 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 12, 2004, 08:08:00 ; Search time 37 Seconds  
(without alignments)  
20.793 Million cell updates/sec

Title: US-09-185-908-1  
Perfect score: 23  
Sequence: 1 WXXXXXXG 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 11832

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	65.2	41	2	hemoglobin AI - tu
2	15	65.2	43	2	hypothetical prote
3	14	60.9	9	2	delta sleep-induci
4	14	60.9	11	2	T-cell receptor ga
5	14	60.9	11	2	T-cell receptor ga
6	14	60.9	20	2	T-cell receptor be
7	14	60.9	27	2	AP24 protein - tom
8	14	60.9	27	2	amylase / pullulan
9	14	60.9	34	2	cellulase (BC 3.2.
10	14	60.9	37	2	osmotin I - common
11	14	60.9	37	2	thumatin homolog
12	14	60.9	40	2	photosystem II cen
13	14	60.9	40	2	photosystem II pro
14	14	60.9	41	2	hemoglobin BIII -
15	14	60.9	50	2	photosystem II pro
16	14	60.9	50	2	hypothetical prote
17	13	56.5	18	2	probable cold stre
18	13	56.5	19	2	DNA topoisomerase
19	13	56.5	21	2	T-cell receptor ga
20	13	56.5	21	2	major outer membra
21	13	56.5	21	2	carbonic anhydrase
22	13	56.5	22	2	osmotin homolog -
23	13	56.5	22	2	formalin adhesin C
24	13	56.5	23	2	virg 6 protein - Bo
25	13	56.5	23	2	alkaline trypsin-1
26	13	56.5	24	2	virB protein - Agr
27	13	56.5	26	2	phospholipase A2 (
28	13	56.5	28	2	phospholipase A2 (
29	13	56.5	28	2	phospholipase A2 (

30	13	56.5	30	2	S68639
31	13	56.5	30	2	S68640
32	13	56.5	30	2	H97596
33	13	56.5	31	2	S31075
34	13	56.5	34	2	S68880
35	13	56.5	35	2	H84214
36	13	56.5	35	2	D85762
37	13	56.5	36	2	A81740
38	13	56.5	37	2	S71912
39	13	56.5	37	2	PC1121
40	13	56.5	37	2	S54441
41	13	56.5	38	2	A39558
42	13	56.5	38	2	S40096
43	13	56.5	39	2	S01813
44	13	56.5	39	2	S71913
45	13	56.5	39	2	S73309

ALIGNMENTS

RESULT 1

S01807  
hemoglobin AI - tube worm (Lamellibrachia sp.) (fragment)  
C;Species: Lamellibrachia sp.  
C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 04-Mar-2000  
C;Accession: S01807  
R;Suzuki, T.; Takagi, T.; Ohta, S.  
Biochem. J. 255, 541-545, 1988  
A;Title: N-terminal amino acid sequence of the deep-sea tube worm haemoglobin remarkab  
A;Reference number: S01807; PMID:89076216; PMID:3202832  
A;Accession: S01807  
A;Molecule type: protein  
A;Residues: 1-41 <SUZ>  
C;Superfamily: globin; globin homology  
C;Keywords: oxygen carrier

Query Match 65.2%; Score 15; DB 2; Length 41;  
Best Local Similarity 25.0%; Pred. No. 1.6e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
DB 15 WASVYSSG 22

RESULT 2

A97416  
hypothetical protein AGR\_C\_830 [imported] - Agrobacterium tumefaciens (strain C58, Ceri  
C;Species: Agrobacterium tumefaciens  
C;Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 18-Nov-2002  
C;Accession: A97416  
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldmai  
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B  
Science 294, 2323-2328, 2001  
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium t  
A;Reference number: A97359; PMID:21608551; PMID:11743194  
A;Accession: A97416  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-43 <KUR>  
A;Cross-references: GB:AE007869; PIDN:AAK86282.1; PID:G15155394; GSPDB:GN00169  
C;Genetics:  
A;Gene: AGR\_C\_830  
A;Map position: circular chromosome

Query Match 65.2%; Score 15; DB 2; Length 43;  
Best Local Similarity 25.0%; Pred. No. 1.7e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
DB 20 WTWTKSAG 27

<p>QY 1 WXXXXXXG 8</p> <p>DB 3 WAGDSSG 10</p>		<p>QY 1 WXXXXXXG 8</p> <p>DB 3 WAGDSSG 10</p>	
<p>RESULT 6</p> <p>F49048</p> <p>T-cell receptor beta chain V region (CDR3 junction, clone Vbeta20.1) - human (fragment)</p> <p>C:Species: Homo sapiens (man)</p> <p>C&gt;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997</p> <p>C:Accession: F49048</p> <p>R:Sioud, M.; Kjeldsen-Kragh, J.; Suleyman, S.; Vinje, O.; Natvig, J.B.; Forre, O.</p> <p>Eur. J. Immunol. 22, 2413-2418, 1992</p> <p>A:Title: Limited heterogeneity of T cell receptor variable region gene usage in juvenile</p> <p>A:Reference number: A49048; MUID:92387250; PMID:1387614</p> <p>A:Accession: F49048</p> <p>A&gt;Status: preliminary; not compared with conceptual translation</p> <p>A:Molecule type: mRNA</p> <p>A:Residues: 1-20 &lt;SIO&gt;</p> <p>A:Experimental source: patient SS, IL-2R+ synovial T-cells</p> <p>A&gt;Note: sequence extracted from NCBI backbone (NCBIP:113268)</p> <p>C:Superfamily: immunoglobulin V region; immunoglobulin homology</p> <p>C:Keywords: T-cell receptor</p>		<p>Query Match 60.9%; Score 14; DB 2; Length 20;</p> <p>Best Local Similarity 25.0%; Pred. No. 1.9e+03;</p> <p>Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;</p>	
<p>QY 1 WXXXXXXG 8</p> <p>DB 9 WSATGVYG 16</p>		<p>QY 1 WXXXXXXG 8</p> <p>DB 9 WSATGVYG 16</p>	
<p>RESULT 7</p> <p>PQ0170</p> <p>AP24 protein - tomato (fragment)</p> <p>C:Species: Lycopersicon esculentum (tomato)</p> <p>C&gt;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 28-Apr-1995</p> <p>C:Accession: PQ0170</p> <p>R:Woloshuk, C.P.; Meulenhoff, J.S.; Sela-Buurlage, M.; van den Elzen, P.J.M.; Cornelia</p> <p>Plant Cell 3, 619-628, 1991</p> <p>A:Title: Pathogen-induced proteins with inhibitory activity toward Phytophthora infest</p> <p>A:Reference number: PQ0169; MUID:93044502; PMID:1841721</p> <p>A:Accession: PQ0170</p> <p>A:Molecule type: protein</p> <p>A:Residues: 1-27 &lt;WOL&gt;</p> <p>A:Experimental source: cv. Moneymaker</p> <p>C:Comment: This protein causes lysis of sporangia and growth inhibition of Phytophthora</p> <p>C:Superfamily: thaumatin I</p>		<p>Query Match 60.9%; Score 14; DB 2; Length 27;</p> <p>Best Local Similarity 25.0%; Pred. No. 2.4e+03;</p> <p>Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;</p>	
<p>QY 1 WXXXXXXG 8</p> <p>DB 14 WAATPIG 21</p>		<p>QY 1 WXXXXXXG 8</p> <p>DB 14 WAATPIG 21</p>	
<p>RESULT 8</p> <p>S69372</p> <p>amylase / pullulanase - Bacillus circulans (fragment)</p> <p>C:Species: Bacillus circulans</p> <p>C&gt;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998</p> <p>C:Accession: S69372</p> <p>R:Kim, C.H.; Kim, Y.S.</p> <p>Eur. J. Biochem. 227, 687-693, 1995</p> <p>A:Title: Substrate specificity and detailed characterization of a bifunctional amylase</p> <p>A:Reference number: S69372; MUID:95172052; PMID:7532585</p> <p>A:Accession: S69372</p> <p>A:Molecule type: protein</p> <p>A:Residues: 1-27 &lt;KIM&gt;</p> <p>A&gt;Note: the sequence from Fig. 1 is inconsistent with that from abstract in having 23</p>		<p>Query Match 60.9%; Score 14; DB 2; Length 11;</p> <p>Best Local Similarity 25.0%; Pred. No. 1.2e+03;</p> <p>Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;</p>	
<p>QY 1 WXXXXXXG 8</p> <p>DB 3 WAGDSSG 10</p>		<p>QY 1 WXXXXXXG 8</p> <p>DB 3 WAGDSSG 10</p>	
<p>RESULT 5</p> <p>I41946</p> <p>T-cell receptor gamma chain (5t.1) - mouse (fragment)</p> <p>C:Species: Mus musculus (house mouse)</p> <p>C&gt;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999</p> <p>C:Accession: I41946</p> <p>R:Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.</p> <p>Mol. Cell. Biol. 11, 5902-5909, 1991</p> <p>A:Title: Rearrangement and functional-site sequence analyses of T-cell receptor gamma ge</p> <p>A:Reference number: A41946; MUID:92049316; PMID:1658619</p> <p>A:Accession: I41946</p> <p>A&gt;Status: preliminary; not compared with conceptual translation</p> <p>A:Molecule type: DNA</p> <p>A:Residues: 1-11 &lt;WHE&gt;</p> <p>C:Keywords: T-cell receptor</p>		<p>Query Match 60.9%; Score 14; DB 2; Length 11;</p> <p>Best Local Similarity 25.0%; Pred. No. 1.2e+03;</p> <p>Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;</p>	
<p>QY 1 WXXXXXXG 8</p> <p>DB 3 WAGDSSG 10</p>		<p>QY 1 WXXXXXXG 8</p> <p>DB 3 WAGDSSG 10</p>	
<p>RESULT 4</p> <p>C38887</p> <p>T-cell receptor gamma chain (5a.3) - mouse (fragment)</p> <p>C:Species: Mus musculus (house mouse)</p> <p>C&gt;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999</p> <p>C:Accession: C38887</p> <p>R:Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.</p> <p>Mol. Cell. Biol. 11, 5902-5909, 1991</p> <p>A:Title: Rearrangement and functional-site sequence analyses of T-cell receptor gamma ge</p> <p>A:Reference number: A41946; MUID:92049316; PMID:1658619</p> <p>A:Accession: C38887</p> <p>A&gt;Status: preliminary; not compared with conceptual translation</p> <p>A:Molecule type: DNA</p> <p>A:Residues: 1-11 &lt;WHE&gt;</p> <p>C:Keywords: T-cell receptor</p>		<p>Query Match 60.9%; Score 14; DB 2; Length 11;</p> <p>Best Local Similarity 25.0%; Pred. No. 1.2e+03;</p> <p>Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;</p>	
<p>QY 1 WXXXXXXG 8</p> <p>DB 1 WAGDSSG 8</p>		<p>QY 1 WXXXXXXG 8</p> <p>DB 1 WAGDSSG 8</p>	
<p>RESULT 3</p> <p>QDRB</p> <p>delta sleep-inducing peptide - rabbit</p> <p>C:Species: Oryctolagus cuniculus (domestic rabbit)</p> <p>C&gt;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000</p> <p>C:Accession: A01422</p> <p>R:Monnier, M.; Dudler, L.; Gachter, R.; Maier, P.F.; Tobler, H.J.; Schoenenberger, G.A.</p> <p>Experientia 33, 548-552, 1977</p> <p>A:Title: The delta sleep inducing peptide (DSIP). Comparative properties of the original</p> <p>A:Reference number: A01422; MUID:77185324; PMID:862769</p> <p>A:Accession: A01422</p> <p>A:Molecule type: protein</p> <p>A:Residues: 1-9 &lt;MON&gt;</p> <p>C:Comment: This peptide was obtained from dialysates of occipital venous sinus blood fro</p> <p>C:Superfamily: unassigned animal peptides</p>		<p>Query Match 60.9%; Score 14; DB 2; Length 9;</p> <p>Best Local Similarity 25.0%; Pred. No. 2.8e+05;</p> <p>Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;</p>	
<p>QY 1 WXXXXXXG 8</p> <p>DB 1 WAGDSSG 8</p>		<p>QY 1 WXXXXXXG 8</p> <p>DB 1 WAGDSSG 8</p>	

Query Match 60.9%; Score 14; DB 2; Length 27;  
Best Local Similarity 25.0%; Pred. No. 2.4e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
Db 15 WAAGIVTG 22

## RESULT 9

S13662  
Cellulase (EC 3.2.1.4) - fungus (Sclerotinia sclerotiorum) (fragment)  
N;Alternate names: endo-1,4-beta-glucanase  
C;Species: Sclerotinia sclerotiorum  
C;Date: 19-Mar-1997 #sequence\_revision 21-Nov-1998 #text\_change 21-Nov-1998  
C;Accession: S13662

R;Waksman, G.  
Biochim. Biophys. Acta 1073, 49-55, 1991  
A;Title: Purification and characterization of two endo-beta-1,4-D-glucanases from Sclerotinia sclerotiorum  
A;Reference number: S13662; PMID:91120823; PMID:1991146  
A;Accession: S13662

A;Molecule type: protein  
A;Residues: 1-34 <BIO>  
A;Experimental source: strain de Bary  
C;Function:  
A;Pathway: cellulose degradation  
C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 60.9%; Score 14; DB 2; Length 34;  
Best Local Similarity 25.0%; Pred. No. 2.8e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
Db 8 WIGASEG 15

## RESULT 10

D44957  
osmotin I - common tobacco (cv. Samsun NN) (fragment)  
C;Species: Nicotiana tabacum (common tobacco)

C;Date: 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 12-Apr-1995  
C;Accession: D44957  
R;Takeda, S.; Sato, F.; Ida, K.; Yamada, Y.

Plant Cell Physiol. 31, 215-221, 1990  
A;Title: Characterization of polypeptides that accumulate in cultured Nicotiana tabacum  
A;Reference number: A44957

A;Accession: D44957  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-37 <TAK>  
C;Superfamily: thaumatin I

Query Match 60.9%; Score 14; DB 2; Length 37;  
Best Local Similarity 25.0%; Pred. No. 3e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
Db 14 WAASTPIG 21

## RESULT 11

S17684

thaumatin homolog 2 - barley

C;Species: Hordeum vulgare (barley)

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997  
C;Accession: S17684

R;Hejgaard, J.; Jacobsen, S.; Svendsen, I.  
FEBS Lett. 291, 127-131, 1991

A;Title: Two antifungal thaumatin-like proteins from barley grain.  
A;Reference number: S17573; PMID:92037994; PMID:1936240

A;Accession: S17684

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-37 <HEJ>

C;Superfamily: thaumatin I

Query Match 60.9%; Score 14; DB 2; Length 37;  
Best Local Similarity 25.0%; Pred. No. 3e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
Db 14 WAAAVPAG 21

## RESULT 12

T06869

photosystem II center protein psbJ - Cyanophora paradoxa cyanelle

C;Species: cyanelle Cyanophora paradoxa

C;Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 26-Aug-1999

C;Accession: T06869

R;Stirewalt, V.L.; Michalowski, C.B.; Luffelhardt, W.; Bohnert, H.J.; Bryant, D.A.  
submitted to the EMBL Data Library, July 1995

A;Description: Nucleotide sequence of the cyanelle genome from Cyanophora paradoxa.  
A;Reference number: Z15840

A;Accession: T06869

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-40 <STI>

A;Cross-references: EMBL:U30821; NID:g1016083; PIDN:AAA81212.1; PID:g1016125

A;Experimental source: strain Pringsheim LB555

C;Genetics:

A;Genome: cyanelle

A;Note: psbJ

C;Superfamily: photosystem II protein psbJ

C;Keywords: cyanelle; photosynthesis; photosystem II; thylakoid

Query Match 60.9%; Score 14; DB 2; Length 40;  
Best Local Similarity 25.0%; Pred. No. 3.1e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
Db 11 WLVAIVAG 18

## RESULT 13

AI2286

photosystem II protein J [imported] - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002

C;Accession: AI2286

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriugu

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,

DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A

A;Reference number: AB1807; PMID:21595285; PMID:11759840

A;Accession: AI2286

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-40 <KUR>

A;Cross-references: GB:BA000019; PIDN:BA075547.1; PID:g17132982; GSPDB:GN00179

A;Experimental source: strain PCC 7120

C;Genetics:

A;Gene: psbJ

C;Superfamily: photosystem II protein psbJ

Query Match 60.9%; Score 14; DB 2; Length 40;  
Best Local Similarity 25.0%; Pred. No. 3.1e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8

Job time : 40 secs

```
Db      11  WWTATAG 18

RESULT 14
S01815
hemoglobin BIII - tube worm (Lamellibrachia sp.) (fragment)
C:Species: Lamellibrachia sp.
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 04-Mar-2000
C:Accession: S01815
R:Suzuki, T.; Takagi, T.; Ohta, S.
Biochem. J. 255, 541-545, 1988
A:Title: N-terminal amino acid sequence of the deep-sea tube worm haemoglobin remarkably
A:Reference number: S01807; MUID:89076216; PMID:3202832
A:Accession: S01815
A:Molecule type: protein
A:Residues: 1-41 <SUZ>
C:Superfamily: globin; globin homology
C:Keywords: oxygen carrier

Query Match      60.9%; Score 14; DB 2; Length 41;
Best Local Similarity 25.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      1  WXXXXXXG 8
Db      15  WAEYGSQ 22

RESULT 15
F82719
hypothetical protein XF1135 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: F82719
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A8515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: F82719
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-50 <SIM>
A:Cross-references: GB:AE003849; GB:AE003849; NID:g9106088; PIDN:AAF83945.1; GSPDB:CN001
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carrier, F
as-Neto, E.; Docena, C.; El-Dorfy, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuranae, E.E.; Laig
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.P.; Marino, C.L.; Marques, M.V.; Martins E
A:Authors: Martins, B.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF1135

Query Match      60.9%; Score 14; DB 2; Length 50;
Best Local Similarity 25.0%; Pred. No. 3.7e+03;
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      1  WXXXXXXG 8
Db      41  WEALFASG 48

Search completed: January 12, 2004, 08:11:02
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 12, 2004, 08:07:57 ; Search time 24 Seconds  
(without alignments)  
15.676 Million cell updates/sec

Title: US-09-185-908-1  
Perfect score: 23  
Sequence: 1 WXXXXXXG 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 4018

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query %	Match	Length	ID	Description
1	15	65.2	34	1	MYTA_MYTD	P81612 mytilus edu
2	15	65.2	41	1	GLB1_LAMSP	P20412 lamellibrac
3	14	60.9	9	1	DSIP_RABIT	P01158 mytilus edu
4	14	60.9	29	1	DMS5_PHYSA	P80281 phyllomedus
5	14	60.9	33	1	RUGA_RANRU	P80954 rana rugosa
6	14	60.9	34	1	GUNI_SCLSC	P21833 sclerotinia
7	14	60.9	35	1	NEP_FVLIH3	P05854 human immun
8	14	60.9	37	1	THRS_HORVU	P33045 hordeum vul
9	14	60.9	39	1	PSBJ_SYN7	P83045 hordeum vul
10	14	60.9	40	1	PSBJ_ANASP	P83045 hordeum vul
11	14	60.9	40	1	PSBJ_CVAPA	P83045 hordeum vul
12	14	60.9	40	1	PSBJ_GINBI	P83045 hordeum vul
13	14	60.9	40	1	PSBJ_SINEL	P83045 hordeum vul
14	13	56.5	17	1	NEP_FVLIJ3	P83045 hordeum vul
15	13	56.5	18	1	TOP1_KLEAE	P83045 hordeum vul
16	13	56.5	24	1	PCL1_PACGO	P83045 hordeum vul
17	13	56.5	24	1	PCL2_PACGO	P83045 hordeum vul
18	13	56.5	26	1	PCW3_PACGO	P83045 hordeum vul
19	13	56.5	28	1	PA22_MICNI	P83045 hordeum vul
20	13	56.5	28	1	PA23_MICNI	P83045 hordeum vul
21	13	56.5	29	1	TLF_ACTDE	P83045 hordeum vul
22	13	56.5	37	1	PIL1_ACHLY	P83045 hordeum vul
23	13	56.5	38	1	PA21_MATBI	P83045 hordeum vul
24	13	56.5	39	1	MCP1_SOLTU	P83045 hordeum vul
25	13	56.5	39	1	PSBJ_GUTHI	P83045 hordeum vul
26	13	56.5	39	1	PSBJ_FORPU	P83045 hordeum vul
27	13	56.5	39	1	PSBJ_SYN2	P83045 hordeum vul
28	13	56.5	40	1	PSBJ_ARYTH	P83045 hordeum vul
29	13	56.5	40	1	PSBJ_HORVU	P83045 hordeum vul
30	13	56.5	40	1	PSBJ_LOTUA	P83045 hordeum vul
31	13	56.5	40	1	PSBJ_MAGTR	P83045 hordeum vul
32	13	56.5	40	1	PSBJ_MAIZE	P83045 hordeum vul
33	13	56.5	40	1	PSBJ_MARPO	P83045 hordeum vul

34	13	56.5	40	1	PSBJ_OENHO	Q9mtk7 oenothera h
35	13	56.5	40	1	PSBJ_ORYSA	P12189 oryza sativ
36	13	56.5	40	1	PSBJ_PEA	P13555 pisum sativ
37	13	56.5	40	1	PSBJ_PINTH	P41618 pinus thum
38	13	56.5	40	1	PSBJ_POPDE	P92417 populus del
39	13	56.5	40	1	PSBJ_PSIU	Q8w106 psilotum nu
40	13	56.5	40	1	PSBJ_SECC	P19053 secale cere
41	13	56.5	40	1	PSBJ_SPIOL	Q9m312 spinacia ol
42	13	56.5	40	1	PSBJ_TOBAC	P12190 nicotiana t
43	13	56.5	42	1	PSBJ_CVAPA	P19153 cyanophora
44	13	56.5	42	1	PSBJ_CHAGL	Q8m9x0 chaetophae
45	13	56.5	42	1	PSBJ_CHLVU	P56338 chlorella v

## ALIGNMENTS

RESULT 1  
MYTA\_MYTD  
AC P81612, STANDARD; PRT; 34 AA.  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Mytilin A.  
OS Mytilus edulis (Blue mussel).  
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloida;  
OC Mytiloidea; Mytilidae; Mytilus.  
OX NCBI\_TaxID=6550;  
RN [1]  
RP SEQUENCE, AND CHARACTERIZATION.  
RC TISSUE=Blood.  
RX MEDLINE=96355569; PubMed=8702979;  
RA Charlet M., Chernysh S., Philippe H., Hetru C., Hoffman J.A.,  
RA Bulet P.;  
RT "Innate immunity. Isolation of several cysteine-rich antimicrobial  
RT peptides from the blood of a mollusc, Mytilus edulis.";  
RL J. Biol. Chem. 271:21808-21813(1996).  
CC -!- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST A.VIRIDANS,  
CC B.MEGATERIUM, M.LUTEUS, E.FAECALIS, S.AUREUS AND E.COLI.  
CC IT IS ACTIVE AGAINST THE MARINE SPECIES A.CARRAGEENOVORA,  
CC P.ALGINOVORA AND C.DROBACHIENSIS.  
CC -!- PTM: THE CYSTEINE RESIDUES PRESUMABLY EXIST IN INTRAMOLECULAR  
CC DISULFIDE BRIDGES.  
CC -!- MASS SPECTROMETRY: MW=3773.7; METHOD=MALDI.  
KW Antibiotic.  
SQ SEQUENCE 34 AA; 3781 MW; P61805D5500CA698 CRC64;

Query Match 65.2%; Score 15; DB 1; Length 34;  
Best Local Similarity 25.0%; Pred. No. 6.2e+02;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
Db 18 WASASFRG 25

RESULT 2  
GLB1\_LAMSP  
AC P20412, STANDARD; PRT; 41 AA.  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Giant hemoglobin AI chain (Fragment).  
OS Lamellibrachia sp. (Deep-sea giant tube worm).  
OC Eukaryota; Metazoa; Pogonophora; Vestimentifera; Basibranchia;  
OC Lamellibrachia; Lamellibrachidae; Lamellibrachia.  
OX NCBI\_TaxID=6424;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=89076216; PubMed=3202832;  
RA Suzuki T., Takagi T., Ohta S.;

RT "N-terminal amino acid sequence of the deep-sea tube worm haemoglobin  
RT remarkably resembles that of annelid haemoglobin.";  
RL Biochem J. 255:541-545(1988).  
CC -1- SUBUNIT: GIANT HEMOGLOBIN IS COMPOSED OF FOUR HEME-CONTAINING  
CC CHAINS (AI TO AIV), AND TWO LINKER CHAINS (AV AND AVI).  
CC -1- SIMILARITY: Belongs to the globin family.

CC PIR: S01807; S01807.  
DR InterPro: IPR000971; Globin.  
DR Pfam: PF00042; Globin; 1.  
DR PROSITE: PS01033; GLOBIN; PARTIAL.  
KW Heme; Oxygen transport; Transport.  
FT NON TER 41  
SQ SEQUENCE 41 AA; 4572 MW; 673E6629936FA5D9 CRC64;  
Query Match 65.2%; Score 15; DB 1; Length 41;  
Best Local Similarity 25.0%; Pred. No. 7.2e+02;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
DB 15 WASVYSSG 22

RESULT 3  
ID DSIP RABIT STANDARD; PRT; 9 AA.  
AC P01158;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Delta sleep-inducing peptide (DSIP).  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=77185324; PubMed=862769;  
RA Monnier M., Dudley L., Gachter R., Maier P.F., Tobler H.J.,  
RA Schoenenberger G.A.;  
RT "The delta sleep inducing peptide (DSIP). Comparative properties of  
RT the original and synthetic nonapeptide.";  
RL Experientia 33:548-552(1977).  
RN [2]  
RP SEQUENCE, AND SYNTHESIS.  
RX MEDLINE=79054421; PubMed=568769;  
RA Schoenenberger G.A., Maier P.F., Tobler H.J., Wilson K., Monnier M.;  
RT "The delta EEG (sleep)-inducing peptide (DSIP). XI. Amino-acid  
RT analysis, sequence, synthesis and activity of the nonapeptide.";  
RL Pflugers Arch. 376:119-129(1978).  
RN [3]  
RP REVIEW.  
RX MEDLINE=87175129; PubMed=3550726;  
RA Graf M.V., Kastin A.J.;  
RT "Delta-sleep-inducing peptide (DSIP): an update.";  
RL Peptides 7:1165-1187(1986).  
CC -1- FUNCTION: WHEN INFUSED INTO THE MESODIENCEPHALIC VENTRICLE OF  
CC RECIPIENT RABBITS INDUCES SPINDLE AND DELTA EEG ACTIVITY AND  
CC REDUCED MOTOR ACTIVITIES.  
CC -1- MISCELLANEOUS: THIS PEPTIDE WAS OBTAINED FROM DIALYSATES OF  
CC OCCIPITAL VENOUS SINUS BLOOD FROM RABBITS KEPT ASLEEP BY ELECTRIC  
CC STIMULATION OF THE THALAMUS.  
CC -1- DATABASE: NAME=Protein Spotlight;  
CC NOTE=Issue 8 of March 2001;  
CC WWW="http://www.expasy.org/spotlight/articles/spltt008.html".  
DR PIR: A01422; QDRB.  
SQ SEQUENCE 9 AA; 849 MW; DDD365BDDAA8787D CRC64;

Query Match 60.9%; Score 14; DB 1; Length 9;  
Best Local Similarity 25.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 WXXXXXXG 8

Db 1 WAGGDASG 8

## RESULT 4

ID DMS5\_PHYSA STANDARD; PRT; 29 AA.  
AC P80281;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Dermaseptin 5 (DS V).  
OS Phyllomedusa sauvagii (Savage's leaf frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
OC Phyllomedusinae; Phyllomedusa.  
OX NCBI\_TaxID=8395;  
RN [1]  
RP SEQUENCE.  
RX TISSUE=Skin secretion;  
RX MEDLINE=94139686; PubMed=8306981;  
RA Mor A., Nicolas P.;  
RT "Isolation and structure of novel defensive peptides from frog skin.";  
RL Eur. J. Biochem. 219:145-154(1994).  
CC -1- FUNCTION: POSSESSES A POTENT ANTIMICROBIAL ACTIVITY AGAINST  
CC BACTERIA FUNGI AND PROTOZOA. PROBABLY ACTS BY DISTURBING MEMBRANE  
CC FUNCTIONS WITH ITS AMPHIPATHIC STRUCTURE.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Skin.  
CC -1- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.  
CC Dermaseptin subfamily.  
KW Amphibian defense peptide; Antibiotic; Fungicide; Multigene family.  
SQ SEQUENCE 29 AA; 2840 MW; 540A4971FC5BB506 CRC64;  
Query Match 60.9%; Score 14; DB 1; Length 29;  
Best Local Similarity 25.0%; Pred. No. 1.1e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
DB 3 WSKIRTAG 10

## RESULT 5

ID RUGA\_RANRU STANDARD; PRT; 33 AA.  
AC P80954;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Rugosin A.  
OS Rana rugosa (Wrinkled frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.  
OX NCBI\_TaxID=8410;  
RN [1]  
RP SEQUENCE.  
RX TISSUE=Skin secretion;  
RX MEDLINE=95336450; PubMed=7612013;  
RA Suzuki S., Ohe Y., Kagegawa T., Tatemoto K.;  
RT "Isolation and characterization of novel antimicrobial peptides,  
RT rugosins A, B and C, from the skin of the frog, Rana rugosa.";  
RL Biochem. Biophys. Res. Commun. 212:249-254(1995).  
CC -1- FUNCTION: Has antibacterial activity against Gram-positive  
CC bacteria.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: SKIN.  
CC -1- SIMILARITY: Belongs to the brevinin family.  
KW Amphibian defense peptide; Antibiotic.  
FT DISULFID 27  
SQ SEQUENCE 33 AA; 3440 MW; E41DA4CF3916CA4C CRC64;  
Query Match 60.9%; Score 14; DB 1; Length 33;

Best Local Similarity 25.0%; Pred. No. 1.2e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
DB 9 WATSIAGK 16

## RESULT 6

GUNI\_SCLSC  
ID GUN1\_SCLSC STANDARD; PRT; 34 AA.  
AC P21833;  
DT 01-MAY-1991 (Rel. 18, Created)  
DT 01-MAY-1991 (Rel. 18, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Endoglucanase 1 (EC 3.2.1.4) (Endo-1,4-beta-glucanase) (Cellulase)  
DE (EG1) (Fragment).  
OS Sclerotinia sclerotiorum.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomyces;  
OC Helotiales; Sclerotiniaceae; Sclerotinia.  
OX NCBI\_TaxID=5180;  
RN [1]  
RP SEQUENCE  
RX MEDLINE=91120823; PubMed=1991146;  
RA Waksman G.;  
RT "Purification and characterization of two endo-beta-1,4-D-glucanases  
from Sclerotinia sclerotiorum";  
RL Biochim. Biophys. Acta 1073:49-55 (1991).  
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic  
linkages in cellulose, lichenin and cereal beta-D-glucans.  
CC -1- MISCELLANEOUS: ACTIVE TOWARDS CARBOXYMETHYL CELLULOSE AND  
4-METHYLBELLIFERYL CELLOBIOSIDE.  
CC -1- SIMILARITY: TO S. COMMUNE EGI.  
DR PIR; S13662; S13662.  
KW Cellulose degradation; Hydrolase; Glycosidase.  
FT NON\_TER 34 34  
SQ SEQUENCE 34 AA; 3452 MW; 9F83ACFF75FC9F78 CRC64;

Query Match 60.9%; Score 14; DB 1; Length 34;  
Best Local Similarity 25.0%; Pred. No. 1.2e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
DB 8 WIGASESG 15

## RESULT 7

NEF\_HV1H3  
ID NEF\_HV1H3 STANDARD; PRT; 35 AA.  
AC P05854;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-NOV-1988 (Rel. 09, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Negative factor (p-protein) (27 kDa protein) (3' ORF) (Fragment).  
GN NEF.  
OS Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1).  
OC Viruses; Retroviruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11707;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85228248; PubMed=2988795;  
RA Crowl R., Ganguly K., Gordon M., Conroy R., Schaber M., Kramer R.,  
Shaw G.M., Wong-Staal F., Reddy E.P.;  
RT "HIV-III env gene products synthesized in E. coli are recognized by  
antibodies present in the sera of AIDS patients.";  
RL Cell 41:979-986 (1985).  
RN [2]  
RP POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.  
RX MEDLINE=88039140; PubMed=3118220;  
RA Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,  
Montagnier L., Lecocq J.-P.;  
RT "HIV F/3' orf encodes a phosphorylated GTP-binding protein resembling

RT an oncogene product".  
RL Nature 330:266-269 (1987).  
CC -1- FUNCTION: NEF has GTPase, GTP-binding and autophosphorylating  
activities. It seems to down-regulate the CD4(T4) antigen.

CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

CC -----  
DR EMBL; M14100; AAA44680.1; --  
DR HIV; M14100; NEFSHXB3.  
DR InterPro; IPR001558; HIV\_Nef.  
DR Pfam; PF00469; F-protein; 1.  
DR ProDom; PD000031; HIV\_Nef; 1.  
KW AIDS; Myristate; GTP-Binding.  
FT LIPID 2 2 MYRISTATE.  
FT NON\_TER 35 35  
SQ SEQUENCE 35 AA; 3714 MW; F66354AFBE1DFCFE CRC64;

Query Match 60.9%; Score 14; DB 1; Length 35;  
Best Local Similarity 25.0%; Pred. No. 1.2e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
DB 5 WSKSSWVG 12

## RESULT 8

THHS\_HORVU  
ID THHS\_HORVU STANDARD; PRT; 37 AA.  
AC P33045;  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 01-OCT-1993 (Rel. 27, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Antifungal protein S (Fragment).  
OS Hordeum vulgare (Barley).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;  
OC Triticeae; Hordeum.  
OX NCBI\_TaxID=4513;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=CV. BOMI RISO 1508;  
RX MEDLINE=92037994; PubMed=1936240;  
RA Heigaard J., Jacobsen S., Svendsen I.;  
RT "Two antifungal thaumatin-like proteins from barley grain.";  
RL FEBS Lett. 291:127-131 (1991).  
CC -1- FUNCTION: HAS ANTIFUNGAL ACTIVITY. INHIBITS THE GROWTH OF  
TRICHODERMA VIRIDAE AND CANDIDA ALBICANS.  
CC -1- SIMILARITY: Belongs to the thaumatin family.  
DR PIR; S17684; S17684.  
DR HSP; P33679; IDU5.  
DR InterPro; IPR001938; Thaumatin.  
DR Pfam; PF00314; Thaumatin; 1.  
DR ProDom; PD001321; Thaumatin; 1.  
DR PROSITE; PS00316; THAUMATIN; PARTIAL.  
KW Plant defense; Fungicide.  
FT NON\_TER 37 37  
SQ SEQUENCE 37 AA; 3871 MW; 7BE164CCBE8A9881 CRC64;

Query Match 60.9%; Score 14; DB 1; Length 37;  
Best Local Similarity 25.0%; Pred. No. 1.3e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WXXXXXXG 8  
DB 14 WAAAVPAG 21

Mon Jan 12 08:42:32 2004

photosystem II; its exact function is not yet known.  
 -1- SIMILARITY: Belongs to the psbJ family.  
 -----  
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).  
 -----  
 EMBL; AP003594; BAB75547.1; --  
 DR PIR; A12286; A12286.  
 DR HAMAP; MF 01305; -; 1.  
 DR InterPro; IPR002682; PSII\_PsbJ.  
 DR Pfam; PF01788; PsbJ; 1.  
 DR ProDom; PD003776; PSII\_PsbJ; 1.  
 KW Photosynthesis; Photosystem II; Reaction center; Transmembrane;  
 FT TRANSMEM 10 32 POTENTIAL.  
 SQ SEQUENCE 40 AA; 3973 MW; 2F6D7354C19A6303 CRC64;  
 Query Match 60.9%; Score 14; DB 1; Length 40;  
 Best Local Similarity 25.0%; Pred. No. 1.4e+03;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 WXXXXXXG 8  
 DB 11 WVATVAG 18  
 RESULT 11  
 PSBJ CYAPA STANDARD; PRT; 40 AA.  
 ID PSBJ CYAPA STANDARD; PRT; 40 AA.  
 AC P19155;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Photosystem II reaction center J protein.  
 GN PSBJ.  
 OS Cyanophora paradoxa.  
 OC Eukaryota; Glaucocystophyceae; Cyanophoraceae; Cyanophora.  
 OX NCBI\_TaxID=2762;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=UTEX LB 555 / Pringsheim;  
 RA Cantrell A., Bryant D.A.;  
 RT "Nucleotide sequence of the genes encoding cytochrome b-559 from the cyanelle genome of Cyanophora paradoxa.";  
 RL Photosyn. Res. 16:65-81(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=UTEX LB 555 / Pringsheim;  
 RA Stirewalt V.L., Michalowski C.B., Loeffelhardt W., Bohnert H.J., Bryant D.A.;  
 RT "Nucleotide sequence of the cyanelle DNA from Cyanophora paradoxa.";  
 RL Plant Mol. Biol. Rep. 13:327-332(1995).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=UTEX LB 555 / Pringsheim;  
 RA Loeffelhardt W., Stirewalt V.L., Michalowski C.B., Annarella M., Farley J.Y., Schlutsky W.M., Chung S., Newmann-Spallart C., Steiner J.M., Jakowitsch J., Bohnert H.J., Bryant D.A.;  
 RT "The complete sequence of the cyanelle genome of Cyanophora paradoxa: the genetic complexity of a primitive plastid.";  
 RL (in) Schenk H.B.A., Herrmann R., Jeon K.W., Mueller N.E., Schwemmler W. (eds.);  
 RL Eukaryotism and Symbiosis, pp.40-48, Springer-Verlag, Heidelberg (1997).  
 CC -1- FUNCTION: This protein is a component of the reaction center of photosystem II; its exact function is not yet known.  
 CC -1- SIMILARITY: Belongs to the psbJ family.

photosystem II; its exact function is not yet known.  
 -1- SIMILARITY: Belongs to the psbJ family.  
 -----  
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).  
 -----  
 EMBL; AY120853; AM82677.1; --  
 DR HAMAP; MF 01305; -; 1.  
 DR InterPro; IPR002682; PSII\_PsbJ.  
 DR Pfam; PF01788; PsbJ; 1.  
 KW Photosynthesis; Photosystem II; Reaction center; Transmembrane.  
 FT TRANSMEM 7 29 POTENTIAL.  
 SQ SEQUENCE 39 AA; 3842 MW; CE55851E75CD63F0 CRC64;  
 Query Match 60.9%; Score 14; DB 1; Length 39;  
 Best Local Similarity 25.0%; Pred. No. 1.3e+03;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 WXXXXXXG 8  
 DB 10 WVATVAG 17  
 RESULT 10  
 PSBJ ANASP STANDARD; PRT; 40 AA.  
 ID PSBJ ANASP STANDARD; PRT; 40 AA.  
 AC Q8YQH9;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Photosystem II reaction center J protein.  
 GN PSBJ OR ASR3848.  
 OS Anabaena sp. (strain PCC 7120).  
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.  
 OX NCBI\_TaxID=103690;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=21595285; PubMed=11759840;  
 RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriiguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimoto S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.;  
 RT "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";  
 RL DNA Res. 8:205-213(2001).  
 CC -1- FUNCTION: This protein is a component of the reaction center of

-----  
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announcement/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch))  
-----  
EMBL; M35129; AAA31698.1; --  
EMBL; U30821; AAA81212.1; --  
PIR; T06869; T06869.  
DR HAMAP; MF\_01305; --; 1.  
DR InterPro; IPR002682; PSII\_PsbJ.  
DR Pfam; PF01788; PsbJ; 1.  
KW Photosynthesis; Photosystem II; Reaction center; Cyanelle;  
KW Transmembrane.  
FT TRANSMEM 10 32 POTENTIAL.  
SQ SEQUENCE 40 AA; 3972 MW; A40746C06B44B5D8 CRC64;  
  
Query Match 60.9%; Score 14; DB 1; Length 40;  
Best Local Similarity 25.0%; Pred. No. 1.4e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
  
QY 1 WXXXXXXG 8  
DB 11 WLVTAVAG 18  
  
RESULT 12  
ID PSBJ\_GINBI STANDARD; PRT; 40 AA.  
AC Q9TH21;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DE 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Photosystem II reaction center J protein.  
GN PSBJ.  
OS Ginkgo biloba (Ginkgo).  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.  
OX NCBI\_TaxID=3311;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99321801; PubMed=10393241;  
RA Kudla J., Bock R.;  
RT "RNA editing in an untranslated region of the Ginkgo chloroplast genome."  
RL Gene 234:81-86(1999).  
CC -!- FUNCTION: This protein is a component of the reaction center of photosystem II; its exact function is not yet known.  
CC -!- SIMILARITY: Belongs to the psbJ family.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announcement/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch))  
-----  
EMBL; AJ130891; CAB61494.1; --  
EMBL; HAMAP; MF\_01305; --; 1.  
DR InterPro; IPR002682; PSII\_PsbJ.  
DR Pfam; PF01788; PsbJ; 1.  
DR ProDom; PD003776; PSII\_PsbJ; 1.  
KW Photosynthesis; Photosystem II; Reaction center; Chloroplast;  
KW Transmembrane.  
FT TRANSMEM 7 29 POTENTIAL.  
SQ SEQUENCE 40 AA; 4197 MW; 4ADC35FF5B0F37A2 CRC64;  
  
Query Match 60.9%; Score 14; DB 1; Length 40;

Best Local Similarity 25.0%; Pred. No. 1.4e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
  
QY 1 WXXXXXXG 8  
DB 11 WLVTAVAG 18  
  
RESULT 13  
ID PSBJ\_SYNEL STANDARD; PRT; 40 AA.  
AC P59087;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DE 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Photosystem II reaction center J protein.  
GN PSBJ OR TSRI544.  
OS Synchococcus elongatus (Thermosynechococcus elongatus).  
OC Bacteria; Cyanobacteria; Chroococcales; Synchococcus.  
OX NCBI\_TaxID=32046;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=BP-1;  
RX MEDLINE=22225144; PubMed=12240834;  
RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S., Watanabe A., Iriiguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;  
RT "Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1";  
RL DNA Res. 9:123-130(2002).  
CC -!- FUNCTION: This protein is a component of the reaction center of photosystem II; its exact function is not yet known.  
CC -!- SIMILARITY: Belongs to the psbJ family.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announcement/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch))  
-----  
EMBL; AP005374; BAC09096.1; --  
EMBL; HAMAP; MF\_01305; --; 1.  
DR InterPro; IPR002682; PSII\_PsbJ.  
DR Pfam; PF01788; PsbJ; 1.  
DR ProDom; PD003776; PSII\_PsbJ; 1.  
KW Photosynthesis; Photosystem II; Reaction center; Transmembrane;  
KW Complete proteome.  
FT TRANSMEM 10 32 POTENTIAL.  
SQ SEQUENCE 40 AA; 4105 MW; 4D05FAA8C690069E CRC64;  
  
Query Match 60.9%; Score 14; DB 1; Length 40;  
Best Local Similarity 25.0%; Pred. No. 1.4e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
  
QY 1 WXXXXXXG 8  
DB 11 WLVTAVAG 18  
  
RESULT 14  
ID NEF\_HVIJ3 STANDARD; PRT; 17 AA.  
AC P12480;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DE 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Negative factor (F-protein) (27 kDa protein) (3'ORF) (Fragment).  
GN NEF.  
OS Human immunodeficiency virus type 1 (JH3 isolate) (HIV-1).  
OC Viruses; Retroviridae; Lentivirus.

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; X78729; -; NOT\_ANNOTATED\_CDS.  
DR HSP; P06612; IYUA.  
DR InterPro; IPR000380; DNA\_topoisomerase.  
DR PROSITE; PS00396; TOPOISOMERASE\_I\_PROK; PARTIAL.  
KW Isomerase; Topoisomerase; DNA-binding.  
FT NON\_TER 1  
SQ SEQUENCE 18 AA; 2043 MW; 8C1C81238F0BEFA4 CRC64;  
Query Match 56.5%; Score 13; DB 1; Length 18;  
Best Local Similarity 25.0%; Pred. No. 1.4e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 WXXXXXXG 8  
DB 4 WSAFFIDG 11  
Search completed: January 12, 2004, 08:08:40  
Job time : 26 secs

CC NCBI\_TaxID=11694;  
CC [1]  
CC SEQUENCE FROM N.A. PubMed=2669897;  
CC MEDLINE=9352108; Hattori N., Inoue J., Sakuma S., Kurimura T., Yoshida M.;  
CC Koniya N., Hattori N., Inoue J., Sakuma S., Kurimura T., Yoshida M.;  
CC "Nucleotide sequences of gag and env genes of a Japanese isolate of  
CC HIV-1 and their expression in bacteria."  
CC AIDS Res. Hum. Retroviruses 5:411-419(1989).  
CC -!- FUNCTION: NEP has GTPase, GTP-binding and autophosphorylating  
CC activities. It seems to down-regulate the CD4(T4) antigen.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; M21138; AAB03527.1; -;  
DR HIV; M21138; NEPSUH3.  
DR InterPro; IPR001558; HIV\_Nef.  
DR Pfam; PF00469; P-protein; 1.  
KW AIDS; Myristate; GTP-binding.  
FT LIPID 2 2 MYRISTATE (BY SIMILARITY).  
FT NON\_TER 17 17  
SQ SEQUENCE 17 AA; 1501 MW; 656B3F26FEB921E CRC64;  
Query Match 56.5%; Score 13; DB 1; Length 17;  
Best Local Similarity 25.0%; Pred. No. 1.4e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 WXXXXXXG 8  
DB 5 WSKRSVVG 12

RESULT 15  
TOP1\_KLEAF  
ID TOP1\_KLEAF STANDARD; PRT; 18 AA.  
AC P46155;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE DNA topoisomerase I (EC 5.99.1.2) (Omega-protein) (Relaxing enzyme)  
DE (Twisting enzyme) (Swivelase) (Fragment).  
GN TOPA.  
OS Klebsiella aerogenes.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Klebsiella.  
OX NCBI\_TaxID=28451;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=NCCTC 418 / ATCC 15380;  
RX MEDLINE=94220019; PubMed=8166630;  
RA Lynch A.S., Tyrrell R., Smerdon S.J., Briggs G.S., Wilkinson A.J.;  
RT "Characterization of the CyeB protein of Klebsiella aerogenes: direct  
RT evidence that N-acetylserine rather than O-acetylserine serves as the  
RT inducer of the cysteine regulon."  
RL Biochem. J. 299:129-136(1994).  
CC -!- FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO THE  
CC CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER.  
CC -!- CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded  
CC DNA, followed by passage and rejoining.  
CC -!- SUBUNIT: Monomer (By similarity).  
CC -!- MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA  
CC BACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK, IN  
CC WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOSPHORUS  
CC AT ONE END OF THE ENZYME-SEVERED DNA STRAND.  
CC -!- SIMILARITY: BELONGS TO THE PROKARYOTIC TYPE I/III TOPOISOMERASE  
CC FAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; X78729; -; NOT\_ANNOTATED\_CDS.  
DR HSP; P06612; IYUA.  
DR InterPro; IPR000380; DNA\_topoisomerase.  
DR PROSITE; PS00396; TOPOISOMERASE\_I\_PROK; PARTIAL.  
KW Isomerase; Topoisomerase; DNA-binding.  
FT NON\_TER 1  
SQ SEQUENCE 18 AA; 2043 MW; 8C1C81238F0BEFA4 CRC64;  
Query Match 56.5%; Score 13; DB 1; Length 18;  
Best Local Similarity 25.0%; Pred. No. 1.4e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 WXXXXXXG 8  
DB 4 WSAFFIDG 11  
Search completed: January 12, 2004, 08:08:40  
Job time : 26 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 12, 2004, 08:08:01 ; Search time 82 Seconds

(without alignments)  
25.176 Million cell updates/sec

Title: US-09-185-908-1

Perfect score: 23

Sequence: 1 WXXXXXXG 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 39761

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	65.2	15	8	O99386 sus scrofa
2	15	65.2	27	4	Q8WUA6 homo sapien
3	15	65.2	27	12	Q9IU41
4	15	65.2	27	12	Q9IU31
5	15	65.2	27	12	Q9IU38
6	15	65.2	27	12	Q9IU15
7	15	65.2	27	12	Q9IU34
8	15	65.2	27	12	Q9IU44
9	15	65.2	27	12	Q9IU46
10	15	65.2	27	12	Q9IU23
11	15	65.2	27	12	Q9IU21
12	15	65.2	27	12	Q9IU27
13	15	65.2	27	12	Q9IU39
14	15	65.2	27	12	Q9IU18
15	15	65.2	27	12	Q9IU35
16	15	65.2	27	12	Q9IU26

17	15	65.2	27	12	Q9IU37	Q9IJ37 hepatitis c
18	15	65.2	27	12	Q9IU25	Q9IJ25 hepatitis c
19	15	65.2	27	12	Q9PX19	Q9PX19 hepatitis c
20	15	65.2	27	12	Q9IIM1	Q9IIM1 hepatitis c
21	15	65.2	27	12	Q9IU14	Q9IJ14 hepatitis c
22	15	65.2	27	12	Q9IU20	Q9IJ20 hepatitis c
23	15	65.2	27	12	Q9IU33	Q9IJ33 hepatitis c
24	15	65.2	27	12	Q9IU36	Q9IJ36 hepatitis c
25	15	65.2	27	12	Q9IU29	Q9IJ29 hepatitis c
26	15	65.2	27	12	Q9IU45	Q9IJ45 hepatitis c
27	15	65.2	27	12	Q9IU12	Q9IJ12 hepatitis c
28	15	65.2	27	12	Q9IU13	Q9IJ13 hepatitis c
29	15	65.2	27	12	Q9IU24	Q9IJ24 hepatitis c
30	15	65.2	27	12	Q9IU38	Q9IJ38 hepatitis c
31	15	65.2	27	12	Q9IU11	Q9IJ11 hepatitis c
32	15	65.2	27	12	Q9IIM0	Q9IJ10 hepatitis c
33	15	65.2	27	12	Q9IU30	Q9IJ30 hepatitis c
34	15	65.2	27	12	Q9IU22	Q9IJ22 hepatitis c
35	15	65.2	27	12	Q9IIM2	Q9IJ42 hepatitis c
36	15	65.2	27	12	Q9IU42	Q9IJ42 hepatitis c
37	15	65.2	31	2	Q93GF8	Q93GF8 staphylococ
38	15	65.2	35	4	O94783	O94783 homo sapien
39	15	65.2	37	12	Q8J202	Q8J202 machupo vir
40	15	65.2	37	12	Q8J204	Q8J204 amapari vir
41	15	65.2	40	15	Q9QGF9	Q9QGF9 human immun
42	15	65.2	42	9	Q9T022	Q9T022 bacterioph
43	15	65.2	43	16	Q8U5K3	Q8U5K3 agrobacteri
44	15	65.2	45	15	Q9QGF1	Q9QGF1 human immun
45	14	60.9	12	15	O41611	O41611 human immun

#### ALIGNMENTS

##### RESULT 1

O99386 PRELIMINARY; PRT; 15 AA.  
AC O99386, 1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DE 01-MAY-1999 (TREMBLrel. 10, Last annotation update)  
DE Cytochrome oxidase subunit 2 (Fragment).  
GN COII.  
OS Sus scrofa (pig).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Periphera blood;  
RX MEDLINE=98403943; PubMed=9734874;  
RA Tartaglia M., Saulle E.;  
RT "Rapid communication: nucleotide sequence of porcine and ovine tRNA (lys) and ATPase8 mitochondrial genes.";  
RL J. Anim. Sci. 76:2207-2208(1998).  
DR EMBL; AF039170; AAD05063.1; -.  
KW Mitochondrion.  
FT NON TER  
SQ SEQUENCE 15 AA; 1788 MW; 2B93E0B6A0588CB3 CRC64;

Query Match 65.2%; Score 15; DB 8; Length 15;  
Best Local Similarity 25.0%; Pred. No. 2e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
Db 8 WSTSMITG 15

##### RESULT 2

Q8WUA6 PRELIMINARY; PRT; 27 AA.  
ID Q8WUA6

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
OC Hepacivirus.  
OX NCBI\_TaxID=11103;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Alberto S.-F.;  
RT "Influence of the dynamics of Hepatitis C virus quasispecies in the  
RL histological outcome of liver transplantation.";  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF221264; AAF77829.1; -  
DR InterPro; IPR002531; HCV NS1.  
DR Pfam; PF01560; HCV NS1; 1.  
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;  
KW Polyprotein; Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 27  
SQ SEQUENCE 27 AA; 2887 MW; D250829C29407A6D CRC64;  
  
Query Match 65.2%; Score 15; DB 12; Length 27;  
Best Local Similarity 25.0%; Pred. No. 3.3e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
  
QY 1 WXXXXXXG 8  
DB 15 WTLFSSG 22  
  
RESULT 5  
Q91J28 PRELIMINARY; PRT; 27 AA.  
ID Q91J28  
AC Q91J28  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Envelope protein (Genome polyprotein) (Fragment).  
OS Hepatitis C virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
OC Hepacivirus.  
OX NCBI\_TaxID=11103;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Alberto S.-F.;  
RT "Influence of the dynamics of Hepatitis C virus quasispecies in the  
RL histological outcome of liver transplantation.";  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF221267; AAF77829.1; -  
DR InterPro; IPR002531; HCV NS1.  
DR Pfam; PF01560; HCV NS1; 1.  
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;  
KW Polyprotein; Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 27  
SQ SEQUENCE 27 AA; 2827 MW; D250828059407A6D CRC64;  
  
Query Match 65.2%; Score 15; DB 12; Length 27;  
Best Local Similarity 25.0%; Pred. No. 3.3e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
  
QY 1 WXXXXXXG 8  
DB 15 WTLFSSG 22  
  
RESULT 6  
Q91J15 PRELIMINARY; PRT; 27 AA.  
ID Q91J15  
AC Q91J15  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Envelope protein (Genome polyprotein) (Fragment).  
OS Hepatitis C virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
OC Hepacivirus.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA TISSUE=Colon;  
RC Strausberg R.;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC020578; AAH20978.1; -  
KW Hypothetical protein.  
FT NON\_TER 1  
FT NON\_TER 27  
SQ SEQUENCE 27 AA; 2799 MW; C737916C1B1A0435 CRC64;  
  
Query Match 65.2%; Score 15; DB 4; Length 27;  
Best Local Similarity 25.0%; Pred. No. 3.3e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
  
QY 1 WXXXXXXG 8  
DB 12 WVSSTLSG 19  
  
RESULT 3  
Q91J41 PRELIMINARY; PRT; 27 AA.  
ID Q91J41  
AC Q91J41  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Envelope protein (Genome polyprotein) (Fragment).  
OS Hepatitis C virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
OC Hepacivirus.  
OX NCBI\_TaxID=11103;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Alberto S.-F.;  
RT "Influence of the dynamics of Hepatitis C virus quasispecies in the  
RL histological outcome of liver transplantation.";  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF221254; AAF77816.1; -  
DR InterPro; IPR002531; HCV NS1.  
DR Pfam; PF01560; HCV NS1; 1.  
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;  
KW Polyprotein; Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 27  
SQ SEQUENCE 27 AA; 2811 MW; D25082905844A14D CRC64;  
  
Query Match 65.2%; Score 15; DB 12; Length 27;  
Best Local Similarity 25.0%; Pred. No. 3.3e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
  
QY 1 WXXXXXXG 8  
DB 15 WTLFSSG 22  
  
RESULT 4  
Q91J31 PRELIMINARY; PRT; 27 AA.  
ID Q91J31  
AC Q91J31  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Envelope protein (Genome polyprotein) (Fragment).  
OS Hepatitis C virus.

OC Hepacivirus.  
OX NCBI\_TaxID=11103;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Alberto S.-F.;  
RT "Influence of the dynamics of Hepatitis C virus quasiespecies in the  
RT histological outcome of liver transplantation.";  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF221280; AAF77842.1; -.  
DR InterPro; IPR002531; HCV NS1.  
DR Pfam; PF01560; HCV NS1; 1.  
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;  
KW Polyprotein; Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 27  
SQ SEQUENCE 27 AA; 2827 MW; D250828059407A6D CRC64;  
  
Query Match 65.2%; Score 15; DB 12; Length 27;  
Best Local Similarity 25.0%; Pred. No. 3.3e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
  
Qy 1 WXXXXXXG 8  
Db 15 WTLFSSG 22

RESULT 7  
Q9IJ34  
ID Q9IJ34 PRELIMINARY; PRT; 27 AA.  
AC Q9IJ34;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Envelope protein (Genome polyprotein) (Fragment).  
OS Hepatitis C virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
OC Hepacivirus.  
OX NCBI\_TaxID=11103;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Alberto S.-F.;  
RT "Influence of the dynamics of Hepatitis C virus quasiespecies in the  
RT histological outcome of liver transplantation.";  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF221261; AAF77823.1; -.  
DR InterPro; IPR002531; HCV NS1.  
DR Pfam; PF01560; HCV NS1; 1.  
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;  
KW Polyprotein; Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 27  
SQ SEQUENCE 27 AA; 2797 MW; D250928159407A6D CRC64;  
  
Query Match 65.2%; Score 15; DB 12; Length 27;  
Best Local Similarity 25.0%; Pred. No. 3.3e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
  
Qy 1 WXXXXXXG 8  
Db 15 WTLFSSG 22

RESULT 8  
Q9IJ44  
ID Q9IJ44 PRELIMINARY; PRT; 27 AA.  
AC Q9IJ44;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Envelope protein (Genome polyprotein) (Fragment).  
OS Hepatitis C virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
OC Hepacivirus.

OX NCBI\_TaxID=11103;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Alberto S.-F.;  
RT "Influence of the dynamics of Hepatitis C virus quasiespecies in the  
RT histological outcome of liver transplantation.";  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF221251; AAF77813.1; -.  
DR InterPro; IPR002531; HCV NS1.  
DR Pfam; PF01560; HCV NS1; 1.  
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;  
KW Polyprotein; Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 27  
SQ SEQUENCE 27 AA; 2827 MW; D250828059407A6D CRC64;  
  
Query Match 65.2%; Score 15; DB 12; Length 27;  
Best Local Similarity 25.0%; Pred. No. 3.3e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
  
Qy 1 WXXXXXXG 8  
Db 15 WTLFSSG 22

RESULT 9  
Q9IJ46  
ID Q9IJ46 PRELIMINARY; PRT; 27 AA.  
AC Q9IJ46;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Envelope protein (Genome polyprotein) (Fragment).  
OS Hepatitis C virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
OC Hepacivirus.  
OX NCBI\_TaxID=11103;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Alberto S.-F.;  
RT "Influence of the dynamics of Hepatitis C virus quasiespecies in the  
RT histological outcome of liver transplantation.";  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF221249; AAF77811.1; -.  
DR InterPro; IPR002531; HCV NS1.  
DR Pfam; PF01560; HCV NS1; 1.  
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;  
KW Polyprotein; Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 27  
SQ SEQUENCE 27 AA; 2827 MW; D250828059407A6D CRC64;  
  
Query Match 65.2%; Score 15; DB 12; Length 27;  
Best Local Similarity 25.0%; Pred. No. 3.3e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
  
Qy 1 WXXXXXXG 8  
Db 15 WTLFSSG 22

RESULT 10  
Q9IJ23  
ID Q9IJ23 PRELIMINARY; PRT; 27 AA.  
AC Q9IJ23;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Envelope protein (Genome polyprotein) (Fragment).  
OS Hepatitis C virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
OC Hepacivirus.  
OX NCBI\_TaxID=11103;

RP SEQUENCE FROM N.A.  
RA Alberto S.-F.;  
RT "Influence of the dynamics of Hepatitis C virus quasispecies in the  
RL histological outcome of liver transplantation.";  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF221268; AAF77830.1; -  
DR InterPro; IPR002531; HCV\_NSI.  
DR Pfam; PF01560; HCV\_NSI; 1.  
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;  
KW Polyprotein; Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 27  
SQ SEQUENCE 27 AA; 2827 MW; D250828059407A6D CRC64;  
Query Match 65.2%; Score 15; DB 12; Length 27;  
Best Local Similarity 25.0%; Pred. No. 3.3e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 WXXXXXXG 8  
Db 15 WTLFSSG 22  
RESULT 13  
Q9IU39 PRELIMINARY; PRT; 27 AA.  
ID Q9IU39;  
AC Q9IU39;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Envelope protein (Genome polyprotein) (Fragment).  
OS Hepatitis C virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
OC Hepacivirus.  
OX NCBI\_TaxID=11103;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Alberto S.-F.;  
RT "Influence of the dynamics of Hepatitis C virus quasispecies in the  
RL histological outcome of liver transplantation.";  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF221256; AAF77818.1; -  
DR InterPro; IPR002531; HCV\_NSI.  
DR Pfam; PF01560; HCV\_NSI; 1.  
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;  
KW Polyprotein; Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 27  
SQ SEQUENCE 27 AA; 2811 MW; C95132805944A14D CRC64;  
Query Match 65.2%; Score 15; DB 12; Length 27;  
Best Local Similarity 25.0%; Pred. No. 3.3e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 WXXXXXXG 8  
Db 15 WTLFSSG 22  
RESULT 14  
Q9IU18 PRELIMINARY; PRT; 27 AA.  
ID Q9IU18;  
AC Q9IU18;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Envelope protein (Genome polyprotein) (Fragment).  
OS Hepatitis C virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
OC Hepacivirus.  
OX NCBI\_TaxID=11103;  
RN [1]  
RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.  
RA Alberto S.-F.;  
RT "Influence of the dynamics of Hepatitis C virus quasispecies in the  
RL histological outcome of liver transplantation.";  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF221272; AAF77834.1; -  
DR InterPro; IPR002531; HCV\_NSI.  
DR Pfam; PF01560; HCV\_NSI; 1.  
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;  
KW Polyprotein; Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 27  
SQ SEQUENCE 27 AA; 2827 MW; D250828059407A6D CRC64;  
Query Match 65.2%; Score 15; DB 12; Length 27;  
Best Local Similarity 25.0%; Pred. No. 3.3e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 WXXXXXXG 8  
Db 15 WTLFSSG 22  
RESULT 11  
Q9IU21 PRELIMINARY; PRT; 27 AA.  
ID Q9IU21;  
AC Q9IU21;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Envelope protein (Genome polyprotein) (Fragment).  
OS Hepatitis C virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
OC Hepacivirus.  
OX NCBI\_TaxID=11103;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Alberto S.-F.;  
RT "Influence of the dynamics of Hepatitis C virus quasispecies in the  
RL histological outcome of liver transplantation.";  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF221274; AAF77836.1; -  
DR InterPro; IPR002531; HCV\_NSI.  
DR Pfam; PF01560; HCV\_NSI; 1.  
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;  
KW Polyprotein; Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 27  
SQ SEQUENCE 27 AA; 2827 MW; D250828059407A6D CRC64;  
Query Match 65.2%; Score 15; DB 12; Length 27;  
Best Local Similarity 25.0%; Pred. No. 3.3e+03;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 WXXXXXXG 8  
Db 15 WTLFSSG 22  
RESULT 12  
Q9IU27 PRELIMINARY; PRT; 27 AA.  
ID Q9IU27;  
AC Q9IU27;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Envelope protein (Genome polyprotein) (Fragment).  
OS Hepatitis C virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
OC Hepacivirus.  
OX NCBI\_TaxID=11103;  
RN [1]  
RP SEQUENCE FROM N.A.

RA Alberto S.-F.;  
RT "Influence of the dynamics of Hepatitis C virus quasispecies in the  
RL histological outcome of liver transplantation.";  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF221277; AAF77839.1; -.  
DR InterPro; IPR002531; HCV\_NSI.  
DR Pfam; PF01560; HCV\_NSI; 1.  
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;  
KW Polyprotein; Transmembrane.  
KW NON\_TER 1  
FT NON\_TER 27 27  
SQ SEQUENCE 27 AA; 2827 MW; D250828059407A6D CRC64;

Query Match 65.2%; Score 15; DB 12; Length 27;

Best Local Similarity 25.0%; Pred. No. 3.3e+03;

Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8

Db 15 WTLFSSG 22

#### RESULT 15

Q91J35 PRELIMINARY; PRT; 27 AA.

ID Q91J35

AC Q91J35;

DT 01-OCT-2000 (TRENBLrel. 15, Created)

DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)

DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)

DE Envelope protein (Genome polyprotein) (Fragment).

OS Hepatitis C virus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

OC Hepacivirus.

OC NCBI\_TaxID=11103;

RN [1]

RP SEQUENCE FROM N.A.

RA Alberto S.-F.;

RT "Influence of the dynamics of Hepatitis C virus quasispecies in the

RL histological outcome of liver transplantation.";

RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF221260; AAF77822.1; -.  
DR InterPro; IPR002531; HCV\_NSI.

DR Pfam; PF01560; HCV\_NSI; 1.

KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;

KW Polyprotein; Transmembrane.

FT NON\_TER 1

FT NON\_TER 27 27

SQ SEQUENCE 27 AA; 2827 MW; D250828059407A6D CRC64;

Query Match 65.2%; Score 15; DB 12; Length 27;

Best Local Similarity 25.0%; Pred. No. 3.3e+03;

Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8

Db 15 WTLFSSG 22

Search completed: January 12, 2004, 08:13:23

Job time : 86 secs

! FINDPATTERNS on geneseqp:\* allowing 0 mismatches

1 ! 1 W(K,R)XX(S,A) (Y,F)XG January 12, 2004 10:24 ..  
AAR04585 ck: 2828 len: 513 ! Aar04585 Aquaricine I. 3/2003  
W(K,R)XX(S,A) (Y,F)XG  
W(R)xx(A) (Y)XG  
495: AGYYL WRIYAYSG SGMYE  
1  
AAR13181 ck: 2828 len: 513 ! Aar13181 T.aquaticus Aquaricin 1. 10/1991  
W(K,R)XX(S,A) (Y,F)XG  
W(R)xx(A) (Y)XG  
495: AGYYL WRIYAYSG SGMYE  
1  
AAR67653 ck: 2828 len: 513 ! Aar67653 Aqualysin I. 8/1995  
W(K,R)XX(S,A) (Y,F)XG  
W(R)xx(A) (Y)XG  
495: AGYYL WRIYAYSG SGMYE  
1  
AAR97244 ck: 1074 len: 4,473 ! Aar97244 Virulence gene cluster polypeptide  
W(K,R)XX(S,A) (Y,F)XG  
W(K)xx(A) (F)XG  
1,144: KALAN WKPAAPQG IPORL  
1  
AAW82254 ck: 7849 len: 934 ! Aaw82254 JPl0248575 Seq ID 4. 7/1999  
W(K,R)XX(S,A) (Y,F)XG  
W(R)xx(A) (Y)XG  
79: EDGTV WRSRAYHG KLGKY  
1  
AAY41726 ck: 2066 len: 211 ! Aay41726 Human PRO944 protein sequence. 12/  
W(K,R)XX(S,A) (Y,F)XG  
W(R)xx(S) (Y)XG  
30: TALPQ WRIYSYAG DNIVT  
1  
AAY30337 ck: 9802 len: 1,091 ! Aay30337 Protein encoded by the human DLC-1  
W(K,R)XX(S,A) (Y,F)XG  
W(R)xx(S) (F)XG  
401: NGSVN WRTGSFHG PGHIS  
1  
AAY31650 ck: 884 len: 530 ! Aay31650 Brevibacterium flavum mutant D-3-P  
W(K,R)XX(S,A) (Y,F)XG  
W(K)xx(S) (F)XG  
132: LREGE WKRSSFNG VEIFG  
1  
AAY31651 ck: 6831 len: 345 ! Aay31651 Corynebacterium glutamicum D-3-pho  
W(K,R)XX(S,A) (Y,F)XG  
W(K)xx(S) (F)XG  
132: LREGE WKRSSFNG VEIFG  
1  
AAY31649 ck: 644 len: 530 ! Aay31649 Brevibacterium flavum wild-type D-  
W(K,R)XX(S,A) (Y,F)XG  
W(K)xx(S) (F)XG  
132: LREGE WKRSSFNG VEIFG

1  
AAY38430 ck: 5842 len: 212 ! Aay38430 Human secreted protein. 9/1999  
W(K,R)XX(S,A) (Y,F)XG  
W(R)xx(S) (Y)XG  
30: TALPQ WRIYSYAG DNIVT  
1  
AAY38421 ck: 4249 len: 71 ! Aay38421 Human secreted protein encoded by  
W(K,R)XX(S,A) (Y,F)XG  
W(R)xx(S) (Y)XG  
30: TALPQ WRIYSYAG DNIVT  
1  
AAY36134 ck: 9084 len: 230 ! Aay36134 Human secreted protein #6. 9/1999  
W(K,R)XX(S,A) (Y,F)XG  
W(K)xx(S) (Y)XG  
30: MLLPS WKTSSYVG ASIVT  
1  
AAY36181 ck: 8102 len: 230 ! Aay36181 Human secreted protein #53. 9/1999  
W(K,R)XX(S,A) (Y,F)XG  
W(K)xx(S) (Y)XG  
30: MLLPS WKTSSYVG ASIVT  
1  
AAY06346 ck: 8232 len: 84 ! Aay06346 EGIII-like cellulase (partial sequ  
W(K,R)XX(S,A) (Y,F)XG  
W(K)xx(S) (Y)XG  
54: STDST WKWKSYSY SNIVA  
1  
AAY22645 ck: 6831 len: 345 ! Aay22645 3-PGDH protein, also known as sera  
W(K,R)XX(S,A) (Y,F)XG  
W(K)xx(S) (F)XG  
132: LREGE WKRSSFNG VEIFG  
1  
AAY22646 ck: 644 len: 530 ! Aay22646 Wild type 3-PGDH protein, also kno  
W(K,R)XX(S,A) (Y,F)XG  
W(K)xx(S) (F)XG  
132: LREGE WKRSSFNG VEIFG  
1  
AAY22647 ck: 884 len: 530 ! Aay22647 Mutant 3-PGDH protein, also known  
W(K,R)XX(S,A) (Y,F)XG  
W(K)xx(S) (F)XG  
132: LREGE WKRSSFNG VEIFG  
1  
AAY34536 ck: 9824 len: 951 ! Aay34536 Porphyromonas gingivalis protein P  
W(K,R)XX(S,A) (Y,F)XG  
W(K)xx(S) (F)XG  
576: GMFKP WKPPSPGG NLIMI  
1  
AAY34403 ck: 6251 len: 953 ! Aay34403 Porphyromonas gingivalis protein P  
W(K,R)XX(S,A) (Y,F)XG  
W(K)xx(S) (F)XG  
578: GMFKP WKPPSPGG NLIMI  
1  
AAY13939 ck: 1473 len: 220 ! Aay13939 Human transmembrane protein, HP014:

1	29: CALPM	W(K,R)XX(S,A)(Y,F)XG W(R)XX(A)(F)XG WRVSAFIG	SNIIT	
	AAV12226	ck: 4096 len: 114	! Aay12226 Human 5' EST secreted protein SEQ	
1	30: MLLPS	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG WKTSSVVG	ASIVT	
	AAV12227	ck: 8204 len: 55	! Aay12227 Human 5' EST secreted protein SEQ	
1	30: MLLPS	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG WKTSSVVG	ASIVT	
	AAV04143	ck: 2066 len: 211	! Aay04143 Human Tango-73 protein. 6/1999	
1	30: TALPQ	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(Y)XG WRIYSYAG	DNIVT	
	AAW99653	ck: 2066 len: 211	! Aaw99653 Human senescence factor p23 protein	
1	30: TALPQ	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(Y)XG WRIYSYAG	DNIVT	
	AAW88747	ck: 4456 len: 206	! Aaw88747 Secreted protein encoded by gene 9	
1	192: NLLGG	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(F)XG WKYSSPSG	FLIPP	
	AAW88629	ck: 6151 len: 202	! Aaw88629 Secreted protein encoded by gene 9	
1	22: CALPM	W(K,R)XX(S,A)(Y,F)XG W(R)XX(A)(F)XG WRVTAFIG	SNIIVT	
	AAW86307	ck: 1982 len: 210	! Aaw86307 Kidney injury associated molecule	
1	30: CSLPM	W(K,R)XX(S,A)(Y,F)XG W(R)XX(A)(F)XG WRVTAFIG	SNIIVT	
	AAW72976	ck: 2905 len: 376	! Aaw72976 Rhodobacter sphaeroides adh1 form	
1	316: VTGRV	W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(F)XG WKGSAPFG	ARGRT	
	AAW76765	ck: 2905 len: 376	! Aaw76765 R. sphaeroides Adh1 class III alcoh	
1	316: VTGRV	W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(F)XG WKGSAPFG	ARGRT	
	AAW53841	ck: 4392 len: 120	! Aaw53841 Human colon cancer antigen protein	
1		W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(F)XG		





1	✓	AAB06530	ck: 4356	len: 10	! Aab06530 Claudin-2 cyclic cell adhesion rec	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	C	2: C	WRTSSYVG	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	K	2: D	WRVSAFIG	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	K	✓	AAB06628	ck: 4101	len: 10	! Aab06628 Claudin-3 cyclic cell adhesion rec
1	✓	AAB06539	ck: 4374	len: 10	! Aab06539 Claudin-2 cyclic cell adhesion rec	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG	D	2: K	WRTSSYVG	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	K	2: E	WRVSAFIG	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	K	✓	AAB06636	ck: 2665	len: 8	! Aab06636 Claudin-3 cyclic cell adhesion rec
1	✓	AAB06548	ck: 4384	len: 10	! Aab06548 Claudin-2 cyclic cell adhesion rec	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG	E	2: K	WRTSSYVG	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	K	1:	WRVSAFIG	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	K	✓	AAB06645	ck: 2669	len: 8	! Aab06645 Claudin-4 cell adhesion recognitio
1	✓	AAB06557	ck: 4437	len: 10	! Aab06557 Claudin-2 cyclic cell adhesion rec	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG	K	2: D	WRTSSYVG	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	C	2: C	WRVTAFIG	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	C	✓	AAB06654	ck: 4024	len: 10	! Aab06654 Claudin-4 cyclic cell adhesion rec
1	✓	AAB06566	ck: 4438	len: 10	! Aab06566 Claudin-2 cyclic cell adhesion rec	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG	K	2: E	WRTSSYVG	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	D	2: K	WRVTAFIG	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	D	✓	AAB06663	ck: 4042	len: 10	! Aab06663 Claudin-4 cyclic cell adhesion rec
1	✓	AAB06574	ck: 2954	len: 8	! Aab06574 Claudin-2 cyclic cell adhesion rec	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG	K	1:	WRTSSYVG	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	E	2: K	WRVTAFIG	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	E	✓	AAB06672	ck: 4052	len: 10	! Aab06672 Claudin-4 cyclic cell adhesion rec
1	✓	AAB06583	ck: 2665	len: 8	! Aab06583 Claudin-3 cell adhesion recognitio	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	K	1:	WRVSAFIG	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	E	2: K	WRVTAFIG	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	E	✓	AAB06681	ck: 4105	len: 10	! Aab06681 Claudin-4 cyclic cell adhesion rec
1	✓	AAB06592	ck: 4019	len: 10	! Aab06592 Claudin-3 cyclic cell adhesion rec	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	C	2: C	WRVSAFIG	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	K	2: D	WRVTAFIG	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	K	✓	AAB06690	ck: 4106	len: 10	! Aab06690 Claudin-4 cyclic cell adhesion rec
1	✓	AAB06601	ck: 4037	len: 10	! Aab06601 Claudin-3 cyclic cell adhesion rec	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	D	2: K	WRVSAFIG	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	K	1:	WRVTAFIG	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	K	✓	AAB06698	ck: 2669	len: 8	! Aab06698 Claudin-4 cyclic cell adhesion rec
1	✓	AAB06610	ck: 4047	len: 10	! Aab06610 Claudin-3 cyclic cell adhesion rec	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	E	2: K	WRVSAFIG	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	E	1:	WRVTAFIG	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	E	✓	AAB06764	ck: 2655	len: 8	! Aab06764 Claudin-6/9 cell adhesion recognit:
1	✓	AAB06619	ck: 4100	len: 10	! Aab06619 Claudin-3 cyclic cell adhesion rec	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	E	2: K	WRVSAFIG	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	E	1:	WRVTAFIG	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	E	✓	AAB06764	ck: 2655	len: 8	! Aab06764 Claudin-6/9 cell adhesion recognit:

```

1: WKVTAFIG
) AAB06772 ck: 4003 len: 10 ! Aab06772 Claudin-6/9 cyclic cell adhesion
W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(F)XG
2: C WKVTAFIG C
j AAB06781 ck: 4021 len: 10 ! Aab06781 Claudin-6/9 cyclic cell adhesion
W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(F)XG
2: K WKVTAFIG D
j AAB06789 ck: 4031 len: 10 ! Aab06789 Claudin-6/9 cyclic cell adhesion
W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(F)XG
2: K WKVTAFIG E
j AAB06798 ck: 4084 len: 10 ! Aab06798 Claudin-6/9 cyclic cell adhesion
W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(F)XG
2: D WKVTAFIG K
AAB06806 ck: 4085 len: 10 ! Aab06806 Claudin-6/9 cyclic cell adhesion
W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(F)XG
2: E WKVTAFIG K
AAB06814 ck: 2655 len: 8 ! Aab06814 Claudin-6/9 cyclic cell adhesion
W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(F)XG
1: WKVTAFIG
j AAB06911 ck: 4176 len: 10 ! Aab06911 Claudin cell adhesion recognition
W(K,R)XX(S,A)(Y,F)XG
W(K)XX(S)(Y)XG
1: WKIYSYAG DN
j AAB06916 ck: 2655 len: 8 ! Aab06916 Claudin cell adhesion recognition
W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(F)XG
1: WKVTAFIG
AAY99378 ck: 8102 len: 230 ! Aay99378 Human PRO1356 (UNQ705) amino acid
W(K,R)XX(S,A)(Y,F)XG
W(K)XX(S)(Y)XG
30: MLLPS WKTSSYVG ASIVT
AAY99420 ck: 828 len: 205 ! Aay99420 Human PRO1486 (UNQ755) amino acid
W(K,R)XX(S,A)(Y,F)XG
W(K)XX(S)(F)XG
192: NLLGG WKYSFPG FLIPP
AAY99434 ck: 4773 len: 220 ! Aay99434 Human PRO1488 (UNQ757) amino acid
W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(F)XG
30: CALPM WKVTAFIG NSIVV
AAY84609 ck: 8102 len: 230 ! Aay84609 A human membrane associated organi
W(K,R)XX(S,A)(Y,F)XG
W(K)XX(S)(Y)XG
30: MLLPS WKTSSYVG ASIVT
AAY51675 ck: 2898 len: 211 ! Aay51675 Murine clodin 1 protein. 6/2000
W(K,R)XX(S,A)(Y,F)XG
W(K)XX(S)(Y)XG
30: TALPO WKIYSYAG DNIVT
AAY51676 ck: 6271 len: 230 ! Aay51676 Murine clodin 2 protein. 6/2000
W(K,R)XX(S,A)(Y,F)XG
W(R)XX(S)(Y)XG
30: MLLPN WKTSSYVG ASIVT
AAY51679 ck: 7312 len: 219 ! Aay51679 Murine clodin 3 protein. 6/2000
W(K,R)XX(S,A)(Y,F)XG
W(R)XX(A)(F)XG
29: CALPM WRVSAFIG SSIT
AAY51681 ck: 3382 len: 219 ! Aay51681 Murine clodin 6 protein. 6/2000
W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(F)XG
30: CALPM WKVTAFIG NSIVV
AAY44794 ck: 5085 len: 379 ! Aay44794 P. pastoris Formaldehyde Dehydroge
W(K,R)XX(S,A)(Y,F)XG
W(R)XX(A)(F)XG
318: VTGRV WRGCAFGG IKGRT
AAY44795 ck: 7004 len: 392 ! Aay44795 P. pastoris Formaldehyde Dehydroge
W(K,R)XX(S,A)(Y,F)XG
W(R)XX(A)(F)XG
318: VTGRV WRGCAFGG IKGRT
AAY68679 ck: 2066 len: 211 ! Aay68679 A human molecule associated with :
W(K,R)XX(S,A)(Y,F)XG
W(R)XX(S)(Y)XG
30: TALPO WKIYSYAG DNIVT
AAY76130 ck: 5842 len: 212 ! Aay76130 Human secreted protein encoded by
W(K,R)XX(S,A)(Y,F)XG
W(R)XX(S)(Y)XG
30: TALPO WKIYSYAG DNIVT
AAY53588 ck: 8341 len: 381 ! Aay53588 Hepatitis B virus surface antigen
W(K,R)XX(S,A)(Y,F)XG

```



1	30: MLLPS	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG WKTSSYVG	ASIVT	AAU10875	ck: 9502	len: 1,173	! Aau10875 Penicillium citrinum HMG-CoA reduc
1	ABB90240	ck: 9468	len: 140	! Abb90240 Human polypeptide SEQ ID NO 2616.	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG WKTSSYVG	ASIVT	97: GPONG W(K)xx(S)(F)XG WKWQSFDC DADVL
1	30: MLLPS	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG WKTSSYVG	ASIVT	ABG51536	ck: 709	len: 5,701	! Abg51536 Human liver peptide, SEQ ID No 301
1	ABB91999	ck: 1756	len: 303	! Abb91999 Herbicidally active polypeptide SE	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(Y)XG WKTSSYVG	ASIVT	3,952: NVTLK W(K)xx(A)(Y)XG WKKEPYDG GSKIT
1	15: IPGPK	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(Y)XG WRKVAYGG	MQIGY	ABB56595	ck: 8381	len: 14	! Abb56595 Human SNP related amino acid seque
1	ABB93775	ck: 275	len: 895	! Abb93775 Herbicidally active polypeptide SE	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(F)XG WKTSSYVG	ASIVT	6: MLLPS W(R)xx(S)(Y)XG WRTSSYVG A
1	621: RSQSQ	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(F)XG WKTSSYVG	LPHFT	ABB58144	ck: 7060	len: 7,107	! Abb58144 Drosophila melanogaster polypeptid
1	ABB84912	ck: 8102	len: 230	! Abb84912 Human PRO1356 protein sequence SEQ	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG WKTSSYVG	ASIVT	5,614: SCMLN WRPPSYDG GLKVS
1	30: MLLPS	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG WKVTAFIG	NSIVV	ABB62511	ck: 1032	len: 379	! Abb62511 Drosophila melanogaster polypeptid
1	ABB84935	ck: 4773	len: 220	! Abb84935 Human PRO1488 protein sequence SEQ	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WRIYSYAG	DNIVT	319: VVGRV W(K)xx(A)(F)XG WKSAPFG WRSVS
1	AAU76231	ck: 2066	len: 211	! Aau76231 Human senescence associated epithe	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WRIYSYAG	DNIVT	303: VVIAT W(K)xx(S)(F)XG WKNVSPAG GIDNS
1	AAU83691	ck: 4773	len: 220	! Aau83691 Human PRO protein, Seq ID No 200.	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG WKVTAFIG	NSIVV	AAU43488
1	ABB04707	ck: 8102	len: 230	! Abb04707 Human SP82 protein SEQ ID NO:2. 3/	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG WKTSSYVG	ASIVT	8: PGSSP WRPWAFRG SSTTR
1	AAU10521	ck: 8182	len: 230	! Aau10521 Human CAS981 polypeptide. 2/2002	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG WKTSSYVG	ASIVT	ABG00160
1	30: MLLPS	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG WKTSSYVG	ASIVT	ABG00890	ck: 4548	len: 414	! Abg00890 Novel human diagnostic protein #88
1	AAU10522	ck: 6271	len: 230	! Aau10522 Murine CAS81 polypeptide. 2/2002	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WRTSSYVG	ASIVT	275: ARNTS WRPNAPFG YDLS
1	30: MLLPN	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WRTSSYVG	ASIVT	ABG04118	ck: 4411	len: 437	! Abg04118 Novel human diagnostic protein #41
1	30: MLLPN	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WRTSSYVG	ASIVT	ABG07792	ck: 7746	len: 731	! Abg07792 Novel human diagnostic protein #77

1	407: SINPG	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG WKAFAFIG	AAVPG	1	310: LPGDN	WRVTSYSG	LQORV	1	ABB36684	ck: 709 len: 5,701	! Abb36684 Peptide #4190 encoded by human foe
1	ABG11899	ck: 2706 len: 243	! Abg11899 Novel human diagnostic protein #11	1	3,952: NVTLK	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(Y)XG WKKPAYDG	GSKIT	1	ABB50278	ck: 6154 len: 209	! Abb50278 Claudin 4 ovarian tumour marker pr
1	170: LPGDN	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WRVTSYSG	LQORG	1	30: CALPM	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG WRVTAFIG	SNIVT	1	ABB50279	ck: 1473 len: 220	! Abb50279 Claudin 3 ovarian tumour marker pr
1	ABG11900	ck: 2958 len: 292	! Abg11900 Novel human diagnostic protein #11	1	29: CALPM	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG WRVSAFIG	SNIIIT	1	ABB50396	ck: 6151 len: 202	! Abb50396 Human secreted protein encoded by
1	ABG16462	ck: 7378 len: 473	! Abg16462 Novel human diagnostic protein #16	1	22: CALPM	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG WRVTAFIG	SNIVT	1	ABB50515	ck: 4456 len: 206	! Abb50515 Human secreted protein encoded by
1	388: QPLQS	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG WKVRAFIG	STSQE	1	192: NLLGG	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(F)XG WKYSFSG	FLIPP	1	ABB52752	ck: 9451 len: 665	! Abb52752 Escherichia coli polypeptide SEQ I
1	ABG20671	ck: 3301 len: 570	! Abg20671 Novel human diagnostic protein #20	1	148: FWRVL	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(Y)XG WRFRAYG	QVIVA	1	ABB52903	ck: 2461 len: 361	! Abb52903 Escherichia coli polypeptide SEQ I
1	4: MAL	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(Y)XG WRGSAYAG	FLALA	1	35: DEIKY	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WRVTSYSG	GEFPE	1	ABBI7568	ck: 1476 len: 67	! Abbi7568 Human nervous system related polyp
1	ABG21490	ck: 2706 len: 639	! Abg21490 Novel human diagnostic protein #21	1	47: SWIFR	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG WKVNAFTG	LMYST	1	ABB22021	ck: 709 len: 5,701	! Abb22021 Protein #4020 encoded by probe for
1	230: RPGDN	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WRVTSYSG	LQORG	1	3,952: NVTLK	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(Y)XG WKKPAYDG	GSKIT	1	AAU09178	ck: 8102 len: 230	! Aau09178 Human PRO1356 polypeptide. 1/2002
1	ABG22207	ck: 8207 len: 1,130	! Abg22207 Novel human diagnostic protein #22	1	30: MLLPS	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG WKTSSYVG	ASIVT	1			
1	1,017: AFRCI	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG WKRFSYDG	RWETK	1							
1	ABG27980	ck: 9013 len: 254	! Abg27980 Novel human diagnostic protein #27	1							
1	73: TALPQ	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG WKQSSYAG	DAIIT	1							
1	ABG28241	ck: 8784 len: 1,331	! Abg28241 Novel human diagnostic protein #28	1							
1	1,077: LFLEH	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG WRRWAFRG	PGLPR	1							
1	ABG28410	ck: 9642 len: 5,488	! Abg28410 Novel human diagnostic protein #28	1							
1	2,845: DRPPD	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG WKAGSYLG	QAVKG	1							
1	ABG29205	ck: 7810 len: 1,286	! Abg29205 Novel human diagnostic protein #29	1							



1	AAG90500	ck: 6981	len: 301	! Aag90500 C glutamicum protein fragment SEQ	1	W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(Y)XG	365: EMGLC WKEVAYLG	NEVSD	W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(Y)XG	! Aab71661 Human colon associated protein #9.
1	254: AGRNW	WKLISFTG	IGSVV		1	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(P)XG			W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(F)XG	! Aab71661 Human colon associated protein #9.
1	AAG91161	ck: 9818	len: 530	! Aag91161 C glutamicum protein fragment SEQ	1	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(P)XG	13: RDSGR WREVSFFG	ETERA	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(F)XG	! Aab87565 Human PRO1356. 5/2001
1	132: LREGE	WKGSSPFG	VEIFG		1	W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(F)XG			W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	! Aab87565 Human PRO1356. 5/2001
1	AAB82494	ck: 2905	len: 376	! Aab82494 Rhodobacter sphaeroides formaldehy	1	W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(F)XG			W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	! Aab87565 Human PRO1356. 5/2001
1	316: VTGRV	WKGSAFPG	ARGRT		1	W(K,R)XX(S,A)(Y,F)XG W(R)XX(A)(F)XG			W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(F)XG	! Aab88319 Human membrane or secretory protei
1	AAG75467	ck: 8565	len: 210	! Aag75467 Human colon cancer antigen protein	1	W(K,R)XX(S,A)(Y,F)XG W(R)XX(A)(F)XG			W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(F)XG	! Aab88319 Human membrane or secretory protei
1	31: CALPM	WRVTAFIG	SNIVT		1	W(K,R)XX(S,A)(Y,F)XG W(R)XX(A)(F)XG			W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(F)XG	! Aab88319 Human membrane or secretory protei
1	AAG81335	ck: 587	len: 496	! Aag81335 Human APP protein sequence SEQ ID	1	W(K,R)XX(S,A)(Y,F)XG W(R)XX(A)(Y)XG			W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	! Aab88342 Human membrane or secretory protei
1	4: MAL	WRGSAYAG	FLALA		1	W(K,R)XX(S,A)(Y,F)XG W(R)XX(A)(Y)XG			W(K,R)XX(S,A)(Y,F)XG W(R)XX(A)(Y)XG	! Aab88466 Human membrane or secretory protei
1	AAE04207	ck: 8102	len: 230	! Aae04207 Human gene 10 encoded secreted pro	1	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG			W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	! Aab66127 Protein of the invention #39. 4/20
1	30: MLLPS	WKTSSYVG	ASIVT		1	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG			W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	! Aab66127 Protein of the invention #39. 4/20
1	AAE04228	ck: 9468	len: 140	! Aae04228 Human gene 10 encoded secreted pro	1	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG			W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	! Aab66127 Protein of the invention #39. 4/20
1	30: MLLPS	WKTSSYVG	ASIVT		1	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG			W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	! Aab66127 Protein of the invention #39. 4/20
1	AAE04281	ck: 5423	len: 113	! Aae04281 Human gene 10 encoded secreted pro	1	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG			W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	! Aab66127 Protein of the invention #39. 4/20
1	3: PS	WKTSSYVG	ASIVT		1	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG			W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	! Aab66127 Protein of the invention #39. 4/20
1	AAE04286	ck: 432	len: 56	! Aae04286 Human gene 10 encoded secreted pro	1	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG			W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	! Aab66127 Protein of the invention #39. 4/20
1	6: MLLPS	WKTSSYVG	ASIVT		1	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG			W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	! Aab66127 Protein of the invention #39. 4/20
1	AAB92516	ck: 6755	len: 643	! Aab92516 Human protein sequence SEQ ID NO:1	1	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG			W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	! Aab50968 Human PRO1488 protein. 3/2001
1	632: TLEKR	WKLCAPEG	IKTT		1	W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(F)XG			W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(F)XG	! Aab50968 Human PRO1488 protein. 3/2001
1	AAB95213	ck: 2647	len: 434	! Aab95213 Human protein sequence SEQ ID NO:1	1	W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(F)XG			W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(F)XG	! Aab64401 Amino acid sequence of human intra

1	ABR47946	ck: 8102	len: 230	! ABR47946 Human secreted protein, SEQ ID 837	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(F)XG	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(F)XG	FLIPP	192: NLLGG	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(F)XG	FLIPP
1	30: MLLPS			ASIVT	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(F)XG	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(F)XG	FLIPP	192: NLLGG	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(F)XG	FLIPP
1	ABR48131	ck: 9468	len: 140	! ABR48131 Human secreted protein, SEQ ID 102	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	ASIVT	30: TALPQ	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(Y)XG	DNIVT
1	30: MLLPS			ASIVT	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	DNIVT	30: TALPQ	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(Y)XG	DNIVT
1	ABG74786	ck: 2447	len: 31,267	! ABG74786 Human RGS11 protein. 6/2003	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	ASIVT	192: NLLGG	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(F)XG	FLIPP
1	22,972: NVTLK			GSKIT	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	FLIPP	192: NLLGG	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(F)XG	FLIPP
1	ABU71162	ck: 2066	len: 211	! ABU71162 Human PRO944 protein. 6/2003	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(Y)XG	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(Y)XG	DNIVT	30: TALPQ	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(Y)XG	DNIVT
1	30: TALPQ			DNIVT	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(Y)XG	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(Y)XG	DNIVT	30: TALPQ	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(Y)XG	DNIVT
1	ABU71278	ck: 828	len: 205	! ABU71278 Human PRO1486 protein. 6/2003	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(F)XG	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(F)XG	FLIPP	192: NLLGG	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(F)XG	FLIPP
1	30: CALPM			NSIVV	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(F)XG	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(F)XG	FLIPP	192: NLLGG	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(F)XG	FLIPP
1	ABU71545	ck: 8102	len: 230	! ABU71545 Human secreted polypeptide PRO1356	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	ASIVT	30: MLLPS	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	ASIVT
1	30: MLLPS			ASIVT	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	ASIVT	30: MLLPS	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	ASIVT
1	ABU71991	ck: 8102	len: 230	! ABU71991 Novel human secreted and transmembrane	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	ASIVT	30: MLLPS	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	ASIVT
1	30: MLLPS			ASIVT	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	ASIVT	30: MLLPS	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	ASIVT
1	ABU72148	ck: 8102	len: 230	! ABU72148 Human PRO polypeptide #40. 6/2003	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	ASIVT	30: MLLPS	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	ASIVT
1	30: MLLPS			ASIVT	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	ASIVT	30: MLLPS	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG	ASIVT
1	ABU65619	ck: 2066	len: 211	! ABU65619 Human secreted/transmembrane prote	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(Y)XG	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(Y)XG	DNIVT	30: TALPQ	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(Y)XG	DNIVT
1	30: TALPQ			DNIVT	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(Y)XG	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(Y)XG	DNIVT	30: TALPQ	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(Y)XG	DNIVT
1	ABU65735	ck: 828	len: 205	! ABU65735 Human secreted/transmembrane prote	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(F)XG	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(F)XG	FLIPP	192: NLLGG	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(F)XG	FLIPP



107: HLFY W(R)xx(A) (Y) xG YEEAI  
WRMLAYKG

Databases searched:  
Geneseq-AA, Release 13.0, Released on 19Jun2003, Formatted on 15Jul2003

Total finds: 271  
Total length: 158,726,570  
Total sequences: 1,107,863  
CPU time: 05:28.43

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 12, 2004, 08:21:38 ; Search time 27 Seconds  
(without alignment)

12.537 Million cell updates/sec

Title: US-09-185-908-1

Perfect score: 23

Sequence: 1 WXXXXXXG 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 61971

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/2/iaa/5A COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/iaa/5B COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/iaa/6A COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/iaa/6B COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/iaa/PCTUS COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	56.5	8	US-09-324-541-11	Sequence 11, Appl
2	12	52.2	8	US-08-469-260A-564	Sequence 564, App
3	12	52.2	8	US-08-488-446-564	Sequence 564, App
4	12	52.2	8	US-08-467-344A-564	Sequence 564, App
5	11	47.8	2	US-08-415-099A-1	Sequence 1, Appl
6	11	47.8	2	US-08-451-822A-19	Sequence 19, Appl
7	11	47.8	3	US-07-858-842-5	Sequence 5, Appl
8	11	47.8	3	US-07-960-636B-4	Sequence 4, Appl
9	11	47.8	3	US-08-165-545-8	Sequence 8, Appl
10	11	47.8	3	US-08-165-545-8	Sequence 8, Appl
11	11	47.8	3	US-08-165-545-12	Sequence 12, Appl
12	11	47.8	3	US-08-305-768-27	Sequence 27, Appl
13	11	47.8	3	US-08-256-771-13	Sequence 13, Appl
14	11	47.8	3	US-08-256-771-17	Sequence 17, Appl
15	11	47.8	3	US-08-256-771-21	Sequence 21, Appl
16	11	47.8	3	US-08-433-037-14	Sequence 14, Appl
17	11	47.8	3	US-08-440-504A-1	Sequence 1, Appl
18	11	47.8	3	US-08-381-984-13	Sequence 13, Appl
19	11	47.8	3	US-08-381-984-17	Sequence 17, Appl
20	11	47.8	3	US-08-381-984-21	Sequence 21, Appl
21	11	47.8	3	US-08-871-163-27	Sequence 27, Appl
22	11	47.8	3	US-08-685-589A-89	Sequence 89, Appl
23	11	47.8	3	US-08-685-589A-90	Sequence 90, Appl
24	11	47.8	3	US-08-685-589A-92	Sequence 92, Appl
25	11	47.8	3	US-08-685-589A-93	Sequence 93, Appl
26	11	47.8	3	US-08-685-589A-94	Sequence 94, Appl
27	11	47.8	3	US-08-767-903-27	Sequence 27, Appl

28	11	47.8	3	US-08-590-897A-25	Sequence 25, Appl
29	11	47.8	3	US-08-433-613-1	Sequence 1, Appl
30	11	47.8	3	US-09-461-697-291	Sequence 291, App
31	11	47.8	3	US-09-461-697-405	Sequence 405, App
32	11	47.8	3	US-08-871-561-44	Sequence 44, Appl
33	11	47.8	3	US-09-167-513-6	Sequence 6, Appl
34	11	47.8	3	US-09-149-476-525	Sequence 525, App
35	11	47.8	3	PCT-US95-11724-27	Sequence 27, Appl
36	11	47.8	4	US-07-801-388-6	Sequence 6, Appl
37	11	47.8	4	US-08-061-065-6	Sequence 6, Appl
38	11	47.8	4	US-07-938-436-1	Sequence 1, Appl
39	11	47.8	4	US-07-932-200-1	Sequence 1, Appl
40	11	47.8	4	US-08-159-617-7	Sequence 7, Appl
41	11	47.8	4	US-07-841-997A-32	Sequence 32, Appl
42	11	47.8	4	US-08-165-545-3	Sequence 3, Appl
43	11	47.8	4	US-08-165-545-6	Sequence 6, Appl
44	11	47.8	4	US-08-165-545-7	Sequence 7, Appl
45	11	47.8	4		

#### ALIGNMENTS

RESULT 1  
US-09-324-541-11  
; Sequence 11, Application US/09324541  
; Patent No. 6391855  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
; TITLE OF INVENTION: JUNCTIONAL ADHESION MOLECULE-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.412  
; CURRENT APPLICATION NUMBER: US/09/324,541  
; CURRENT FILING DATE: 1999-06-02  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 11  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Fab fragment directed against claudin cell  
; OTHER INFORMATION: adhesion recognition sequence  
US-09-324-541-11

Query Match 56.5%; Score 13; DB 4; Length 8;  
Best Local Similarity 25.0%; Pred. No. 2.5e+05;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 WXXXXXXG 8  
DB 1 WKIYSYAG 8

RESULT 2  
US-08-469-260A-564  
; Sequence 564, Application US/08469260A  
; Patent No. 6451578  
; GENERAL INFORMATION:  
; APPLICANT: JOHN N. SIMONS  
; APPLICANT: TAMI J. PILOT-MATIAS  
; APPLICANT: GEORGE J. DAWSON  
; APPLICANT: GEORGE G. SCHLAUDER  
; APPLICANT: SURESH M. DESAI  
; APPLICANT: THOMAS P. LEARY  
; APPLICANT: ANTHONY SCOTT MUEHROFF  
; APPLICANT: JAMES C. ERKER  
; APPLICANT: SHERI L. BUIJK  
; APPLICANT: ISA K. MUSHAWAR  
; TITLE OF INVENTION: NON-A. NON-B. NON-C. NON-D. NON-E HEPATITIS  
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE  
; NUMBER OF SEQUENCES: 716

us-09-185-908-1.slim8.ra1

Mon Jan 12 08:42:32 2004

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,260A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 564:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-469-260A-564

Query Match 52.2%; Score 12; DB 4; Length 8;
Best Local Similarity 25.0%; Pred. No. 2.5e+05;
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8
Db 1 WHSGLLGG 8

RESULT 3
US-08-488-446-564
Sequence 564, Application US/08488446
Patent No. 6558898
GENERAL INFORMATION:
APPLICANT: JOHN N. SIMONS
APPLICANT: TAMI J. PILOT-MATIAS
APPLICANT: GEORGE J. DAWSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUEHROFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUIJK
APPLICANT: ISA K. MUSHAWAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,344A
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,550
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:

CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,344A
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,550
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:

Query Match 52.2%; Score 12; DB 4; Length 8;
Best Local Similarity 25.0%; Pred. No. 2.5e+05;
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8
Db 1 WHSGLLGG 8

RESULT 4
US-08-467-344A-564
Sequence 564, Application US/08467344A
Patent No. 6586568
GENERAL INFORMATION:
APPLICANT: JOHN N. SIMONS
APPLICANT: TAMI J. PILOT-MATIAS
APPLICANT: GEORGE J. DAWSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUEHROFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUIJK
APPLICANT: ISA K. MUSHAWAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,344A
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,550
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:

```

TELEPHONE: 708-937-6365  
TELEFAX: 708-938-2623  
INFORMATION FOR SEQ ID NO: 564:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 564:  
US-08-467-344A-564

Query Match 52.2%; Score 12; DB 4; Length 8;  
Best Local Similarity 25.0%; Pred. No. 2.5e+05;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXX 8  
Db 1 WHSGLGG 8

## RESULT 5

US-08-415-099A-1  
Sequence 1, Application US/08415099A  
Patent No. 5789384

## GENERAL INFORMATION:

APPLICANT: Khavinson, V.Kh., Sery, S.V. and Morozov, V.G.  
TITLE OF INVENTION: "Pharmaceutical Dipeptide Compositions and Methods of Use Thereof"

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cytoven

STREET: 10230 N.E. Points Drive, Suite 530

CITY: Kirkland

STATE: Washington

COUNTRY: USA

ZIP: 98033

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette-3.25 inch, 1.44mb storage

COMPUTER: IBM PC/486 Compatible

OPERATING SYSTEM: MS-DOS 5.01

SOFTWARE: Word for Windows 6.0-t

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/415,099A

FILING DATE: 31-MAR-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/271,386

FILING DATE: 06-JUL-1994

APPLICATION NUMBER: 08/026,341

FILING DATE: March 4, 1993

ATTORNEY/AGENT INFORMATION:

NAME: Sundemo, John S.

REGISTRATION NUMBER: 34,446

REFERENCE/DOCKET NUMBER: 15548-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 1-206-889-5804(direct)

TELEFAX: 1-206-822-3644

TELEX:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2 amino acids

TYPE: AMINO

TOPOLOGY: linear

MOLECULE TYPE: peptide

IMMEDIATE SOURCE:

US-08-415-099A-1

## Query Match

Best Local Similarity 47.8%; Score 11; DB 1; Length 2;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
Db 2 W 2

## RESULT 6

US-08-451-822A-19

Sequence 19, Application US/08451822A

Patent No. 5863888

## GENERAL INFORMATION:

APPLICANT: Dionne, Craig A

APPLICANT: Crumley, Greg

APPLICANT: Jaye, Michael C

APPLICANT: Schlensing, Joseph

TITLE OF INVENTION: Fibroblast Growth Factor Receptors

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Rhone-Poulenc Rorer Legal Department

STREET: 500 Arcola Road

CITY: Collegeville

STATE: PA

COUNTRY: USA

ZIP: 19426

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/451,822A

FILING DATE: 26-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/323,430

FILING DATE: 14-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/934,372

FILING DATE: 21-AUG-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/549,587

FILING DATE: 06-JUL-1990

ATTORNEY/AGENT INFORMATION:

NAME: Savitzky, Martin

REGISTRATION NUMBER: 29,699

REFERENCE/DOCKET NUMBER: A0496E

TELECOMMUNICATION INFORMATION:

TELEPHONE: (610) 454-3816

TELEFAX: (610) 454-3808

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 2 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-451-822A-19

## Query Match

Best Local Similarity 47.8%; Score 11; DB 2; Length 2;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1

Db 1 W 1

## RESULT 7

US-07-858-842-5

Sequence 5, Application US/07858842

Patent No. 5314807

## GENERAL INFORMATION:

APPLICANT: Yoshikawa, Masaaki

APPLICANT: Yokoyama, Keiichi

APPLICANT: Hasegawa, Masayasu

APPLICANT: Yasumoto, Ryouchi

APPLICANT: Fujita, Hiroyuki

;; TITLE OF INVENTION: METHOD FOR PRODUCING AN ANGIOTENSIN  
;; NUMBER OF SEQUENCES: 5  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: ARMSTRONG & KUBOVCIK  
;; STREET: 1725 K Street N.W. Suite 1000  
;; CITY: Washington  
;; STATE: District of Columbia  
;; COUNTRY: United States of America  
;; ZIP: 20006  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/07/858,842  
;; FILING DATE: 19920327  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: JP 142283  
;; FILING DATE: 29-MAR-1991  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: JP 298060  
;; FILING DATE: 17-OCT-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Gormley, Mary E.  
;; REGISTRATION NUMBER: 34, 409  
;; REFERENCE/DOCKET NUMBER: 920247  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202) 659-2930  
;; TELEFAX: (202) 887-0357  
;; TELEX: 440142  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 3 amino acids  
;; TYPE: AMINO ACID  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; HYPOTHETICAL: NO  
;; US-07-858-842-5

Query Match 47.8%; Score 11; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;

QY 1 W 1  
DB 3 W 3

RESULT 8  
US-07-960-636B-4  
; Sequence 4, Application US/07960636B  
; Patent No. 5369015  
; GENERAL INFORMATION:  
; APPLICANT: Yoshikawa, Masaaki  
; APPLICANT: Yokoyama, Keiichi  
; APPLICANT: Hasegawa, Masayasu  
; APPLICANT: Yasumoto, Ryouichi  
; APPLICANT: Fujita, Hiroyuki  
; TITLE OF INVENTION: Method for Producing an Angiotensin  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Armstrong, Westerman, Hattori, McLeland &  
; ADDRESSEE: Naughton  
; STREET: 1725 K Street, N.W., Suite 1000  
; CITY: Washington  
; STATE: DC  
; COUNTRY: U.S.A.  
; ZIP: 20006  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/07/960,636B  
;; FILING DATE: 14-OCT-1992  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: JP 298061/1991  
;; FILING DATE: 17-OCT-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Tockman, Albert  
;; REGISTRATION NUMBER: 19722  
;; REFERENCE/DOCKET NUMBER: F1161-2679-A920798  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202) 659-2930  
;; TELEFAX: (202) 887-0357  
;; INFORMATION FOR SEQ ID NO: 4:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 3 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; ORIGINAL SOURCE:  
;; ORGANISM: Mammalian meat, fish, crustaceans  
;; US-07-960-636B-4

Query Match 47.8%; Score 11; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;

QY 1 W 1  
DB 3 W 3

RESULT 9  
US-08-165-545-4  
; Sequence 4, Application US/08165545  
; Patent No. 5424396  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: Antimicrobial Peptide and  
; TITLE OF INVENTION: Antimicrobial Agent  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: DisplayWrite  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/165,545  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/871,981  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:  
LENGTH: 3 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL LINE:  
ORGANELLE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:

US-08-165-545-4

Query Match 47.8%; Score 11; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1  
DB 1 W 1

RESULT 10  
US-08-165-545-8  
Sequence 8, Application US/08165545  
Patent No. 5424396

GENERAL INFORMATION:  
APPLICANT: Mamoru TOMITA et al.  
TITLE OF INVENTION: Antimicrobial Peptide and  
TITLE OF INVENTION: Antimicrobial Agent  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS  
SOFTWARE: DisplayWrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/165,545  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/871,981  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:

INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:

LENGTH: 3 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:

US-08-165-545-8

Query Match 47.8%; Score 11; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1  
DB 2 W 2

RESULT 11  
US-08-165-545-8  
Query Match 47.8%; Score 11; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

us-09-185-908-1.slim8.ra1

Mon Jan 12 08:42:32 2004

US-08-165-545-12  
; Sequence 12, Application US/08165545  
; Patent No. 5424396  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: Antimicrobial peptide and  
; TITLE OF INVENTION: Antimicrobial Agent  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: DisplayWrite  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/165,545  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/871,981  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX:  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE:  
; HYPOTHETICAL:  
; ANTI-SENSE:  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
; ORGANISM:  
; STRAIN:  
; INDIVIDUAL ISOLATE:  
; DEVELOPMENTAL STAGE:  
; HAPLOTYPE:  
; TISSUE TYPE:  
; CELL TYPE:  
; CELL LINE:  
; ORGANELLE:  
; IMMEDIATE SOURCE:  
; LIBRARY:  
; CLONE:  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT:  
; MAP POSITION:  
; UNITS:  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION:  
; PUBLICATION INFORMATION:  
; AUTHORS:  
; TITLE:  
; JOURNAL:  
; VOLUME:  
; ISSUE:

US-08-165-545-12  
; PAGES:  
; DATE:  
; DOCUMENT NUMBER:  
; FILING DATE:  
; PUBLICATION DATE:  
; RELEVANT RESIDUES IN SEQ ID NO:  
US-08-165-545-12  
Query Match 47.8%; Score 11; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 W 1  
Db 2 W 2  
RESULT 12  
US-08-305-768-27  
; Sequence 27, Application US/08305768  
; Patent No. 5602097  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Antifungal Peptides  
; NUMBER OF SEQUENCES: 31  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/305,768  
; FILING DATE: 12-SEPT-1994  
; CLASSIFICATION: 514  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-305-768-27  
Query Match 47.8%; Score 11; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 W 1  
Db 1 W 1  
RESULT 13  
US-08-256-771-13  
; Sequence 13, Application US/08256771  
; Patent No. 5656591  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING  
; TITLE OF INVENTION: PRODUCTS THEREWITH  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1

;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/256,771  
;; FILING DATE: July 22, 1994  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER:  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Warren M. Cheek, Jr.  
;; REGISTRATION NUMBER: 33,367  
;; REFERENCE/DOCKET NUMBER:  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-371-8850  
;; TELEFAX:  
;; TELEX:

;; INFORMATION FOR SEQ ID NO: 13:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 3 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-256-771-13

Query Match 47.8%; Score 11; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1  
|  
DB 1 W 1

RESULT 14  
US-08-256-771-17  
;; Sequence 17, Application US/08256771  
;; Patent No. 5656591  
;; GENERAL INFORMATION:  
;; APPLICANT: Mamoru TOMITA et al.  
;; TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING  
;; NUMBER OF SEQUENCES: 32  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Wenderoth, Lind & Ponack  
;; STREET: 805 Fifteenth Street, N.W., #700  
;; CITY: Washington  
;; STATE: D.C.  
;; COUNTRY: U.S.A.  
;; ZIP: 20005

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: MS-DOS  
;; SOFTWARE: Wordperfect 5.1  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/256,771  
;; FILING DATE: July 22, 1994  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Warren M. Cheek, Jr.  
;; REGISTRATION NUMBER: 33,367  
;; REFERENCE/DOCKET NUMBER:  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-371-8850  
;; TELEFAX:  
;; TELEX:

;; INFORMATION FOR SEQ ID NO: 17:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 3 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-256-771-21

Query Match 47.8%; Score 11; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1  
|  
DB 2 W 2

;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-256-771-17

Query Match 47.8%; Score 11; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1  
|  
DB 2 W 2

RESULT 15  
US-08-256-771-21  
;; Sequence 21, Application US/08256771  
;; Patent No. 5656591  
;; GENERAL INFORMATION:  
;; APPLICANT: Mamoru TOMITA et al.  
;; TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING  
;; NUMBER OF SEQUENCES: 32  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Wenderoth, Lind & Ponack  
;; STREET: 805 Fifteenth Street, N.W., #700  
;; CITY: Washington  
;; STATE: D.C.  
;; COUNTRY: U.S.A.  
;; ZIP: 20005

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: MS-DOS  
;; SOFTWARE: Wordperfect 5.1  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/256,771  
;; FILING DATE: July 22, 1994  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER:  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Warren M. Cheek, Jr.  
;; REGISTRATION NUMBER: 33,367  
;; REFERENCE/DOCKET NUMBER:  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-371-8850  
;; TELEFAX:  
;; TELEX:

;; INFORMATION FOR SEQ ID NO: 21:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 3 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-256-771-21

Query Match 47.8%; Score 11; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1  
|  
DB 2 W 2

Search completed: January 12, 2004, 08:26:47  
Job time : 29 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 12, 2004, 08:25:23 ; Search time 68 seconds

(without alignments)  
23.707 Million cell updates/sec

Title: US-09-185-908-1

Perfect score: 23

Sequence: 1 WXXXXXXG 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747907 seqs, 201509753 residues

Total number of hits satisfying chosen parameters: 49186

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pcp.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pcp.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pcp.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pcp.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pcp.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pcp.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pcp.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pcp.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pcp.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pcp.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pcp.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pcp.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pcp.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pcp.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pcp.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pcp.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pcp.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	14	60.9	8	10 US-09-185-908-42	Sequence 42, Appl
2	14	60.9	8	10 US-09-185-908-163	Sequence 163, App
3	13	56.5	8	10 US-09-185-908-34	Sequence 34, Appl
4	13	56.5	8	10 US-09-185-908-50	Sequence 50, Appl
5	13	56.5	8	10 US-09-185-908-58	Sequence 58, Appl
6	13	56.5	8	10 US-09-185-908-110	Sequence 110, App
7	13	56.5	8	10 US-09-185-908-216	Sequence 216, App
8	13	56.5	8	10 US-09-185-908-269	Sequence 269, App
9	13	56.5	8	11 US-09-986-480-361	Sequence 361, App
10	13	56.5	8	15 US-10-119-537-11	Sequence 11, Appl
11	12	52.2	8	8 US-08-424-550B-564	Sequence 564, App
12	12	52.2	8	12 US-10-231-417-485	Sequence 485, App
13	11	47.8	2	15 US-10-197-954-42	Sequence 42, Appl
14	11	47.8	3	10 US-09-922-261-291	Sequence 291, App
15	11	47.8	3	10 US-09-922-261-405	Sequence 405, App

16	11	47.8	3	10 US-09-982-172-25	Sequence 25, Appl
17	11	47.8	3	11 US-09-809-391-525	Sequence 525, App
18	11	47.8	3	11 US-09-852-910-151	Sequence 151, App
19	11	47.8	3	12 US-10-190-082-239	Sequence 239, App
20	11	47.8	3	12 US-09-882-171-525	Sequence 525, App
21	11	47.8	3	15 US-10-039-876A-6	Sequence 6, Appl
22	11	47.8	4	7 US-08-996-140-6	Sequence 6, Appl
23	11	47.8	4	8 US-08-484-409-5	Sequence 5, Appl
24	11	47.8	4	8 US-08-484-409-29	Sequence 29, Appl
25	11	47.8	4	8 US-08-484-409-34	Sequence 34, Appl
26	11	47.8	4	8 US-08-981-824-43	Sequence 43, Appl
27	11	47.8	4	8 US-08-424-550B-216	Sequence 216, App
28	11	47.8	4	8 US-08-424-550B-314	Sequence 314, App
29	11	47.8	4	8 US-08-424-550B-346	Sequence 346, App
30	11	47.8	4	8 US-08-841-636A-3	Sequence 3, Appl
31	11	47.8	4	9 US-09-736-611-1	Sequence 1, Appl
32	11	47.8	4	9 US-09-736-611-2	Sequence 2, Appl
33	11	47.8	4	9 US-09-765-527-156	Sequence 196, App
34	11	47.8	4	9 US-09-780-070-1	Sequence 1, Appl
35	11	47.8	4	9 US-09-780-070-2	Sequence 2, Appl
36	11	47.8	4	9 US-09-871-212-2	Sequence 2, Appl
37	11	47.8	4	9 US-09-808-037-4	Sequence 4, Appl
38	11	47.8	4	9 US-09-155-076-4	Sequence 4, Appl
39	11	47.8	4	9 US-09-155-076-5	Sequence 5, Appl
40	11	47.8	4	9 US-09-853-918-11	Sequence 11, Appl
41	11	47.8	4	9 US-09-853-918-19	Sequence 19, Appl
42	11	47.8	4	9 US-09-782-980-112	Sequence 112, App
43	11	47.8	4	9 US-09-741-148A-13	Sequence 13, Appl
44	11	47.8	4	9 US-09-682-667-12	Sequence 12, Appl
45	11	47.8	4	9 US-09-682-667-13	Sequence 13, Appl

#### ALIGNMENTS

RESULT 1  
US-09-185-908-42  
; Sequence 42, Application US/09185908A  
; Publication No. US20020193294A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED  
; TITLE OF INVENTION: FUNCTIONS  
; FILE REFERENCE: 100086.409  
; CURRENT APPLICATION NUMBER: US/09/185.908A  
; CURRENT FILING DATE: 1998-11-03  
; NUMBER OF SEQ ID NOS: 269  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 42  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Product of  
; OTHER INFORMATION: synthesis based on mouse claudin-2 sequence  
US-09-185-908-42

Query Match 60.9% Score 14; DB 10; Length 8;  
Best Local Similarity 25.0%; Pred. No. 6.7e+05;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Cy 1 WXXXXXXG 8  
|  
Db 1 WRTSSVVG 8

RESULT 2  
US-09-185-908-163  
; Sequence 163, Application US/09185908A  
; Publication No. US20020193294A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.

```

; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; FILE REFERENCE: 100086.409
; CURRENT APPLICATION NUMBER: US/09/185,908A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 163
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: synthesis based on mouse claudin-2 sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
; OTHER INFORMATION:
US-09-185-908-163

```

```

Query Match 60.9%; Score 14; DB 10; Length 8;
Best Local Similarity 25.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

```

Qy 1 WXXXXXXG 8
|
Db 1 WRTSSYVG 8

```

```

RESULT 3
US-09-185-908-34
; Sequence 34, Application US/09185908A
; Publication No. US20020193294A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; FILE REFERENCE: 100086.409
; CURRENT APPLICATION NUMBER: US/09/185,908A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: Synthesis based on mouse claudin-1 sequence
US-09-185-908-34

```

```

Query Match 56.5%; Score 13; DB 10; Length 8;
Best Local Similarity 25.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

```

Qy 1 WXXXXXXG 8
|
Db 1 WKIYSYAG 8

```

```

RESULT 4
US-09-185-908-50
; Sequence 50, Application US/09185908A
; Publication No. US20020193294A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; FILE REFERENCE: 100086.409
; CURRENT APPLICATION NUMBER: US/09/185,908A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 269

```

```

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: synthesis based on human, mouse and monkey CPE-R
; OTHER INFORMATION: sequences
US-09-185-908-50

```

```

Query Match 56.5%; Score 13; DB 10; Length 8;
Best Local Similarity 25.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

```

Qy 1 WXXXXXXG 8
|
Db 1 WRVTAFIG 8

```

```

RESULT 5
US-09-185-908-58
; Sequence 58, Application US/09185908A
; Publication No. US20020193294A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; FILE REFERENCE: 100086.409
; CURRENT APPLICATION NUMBER: US/09/185,908A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: synthesis based on human and rat RVP-1 sequences
US-09-185-908-58

```

```

Query Match 56.5%; Score 13; DB 10; Length 8;
Best Local Similarity 25.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

```

Qy 1 WXXXXXXG 8
|
Db 1 WRVSAFIG 8

```

```

RESULT 6
US-09-185-908-110
; Sequence 110, Application US/09185908A
; Publication No. US20020193294A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; FILE REFERENCE: 100086.409
; CURRENT APPLICATION NUMBER: US/09/185,908A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 110
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: synthesis based on mouse claudin-1 sequence

```

FEATURE:  
US-09-185-908-110

Query Match 56.5%; Score 13; DB 10; Length 8;  
Best Local Similarity 25.0%; Pred. No. 6.7e+05;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
Db 1 WKIYSYAG 8

## RESULT 7

US-09-185-908-216  
; Sequence 216, Application US/09185908A  
; Publication No. US20020193294A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED  
; FILE REFERENCE: 100086.409  
; CURRENT APPLICATION NUMBER: US/09/185,908A  
; CURRENT FILING DATE: 1998-11-03  
; NUMBER OF SEQ ID NOS: 269  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 216  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Product of  
; OTHER INFORMATION: synthesis based on human, mouse and monkey CPE-R  
; FEATURE:  
; OTHER INFORMATION: Cyclic Peptide  
US-09-185-908-216

Query Match 56.5%; Score 13; DB 10; Length 8;  
Best Local Similarity 25.0%; Pred. No. 6.7e+05;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
Db 1 WRVTAPFG 8

## RESULT 8

US-09-185-908-269  
; Sequence 269, Application US/09185908A  
; Publication No. US20020193294A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED  
; FILE REFERENCE: 100086.409  
; CURRENT APPLICATION NUMBER: US/09/185,908A  
; CURRENT FILING DATE: 1998-11-03  
; NUMBER OF SEQ ID NOS: 269  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 269  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Product of  
; OTHER INFORMATION: synthesis based on human and rat RVP-1 sequences  
; FEATURE:  
; OTHER INFORMATION: Cyclic Peptide  
US-09-185-908-269

Query Match 56.5%; Score 13; DB 10; Length 8;  
Best Local Similarity 25.0%; Pred. No. 6.7e+05;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
Db 1 WRVSAFIG 8

## RESULT 9

US-09-986-480-361  
; Sequence 361, Application US/09986480  
; Publication No. US20030027999A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 143 Human Secreted Proteins  
; FILE REFERENCE: PS500P1  
; CURRENT APPLICATION NUMBER: US/09/986,480  
; CURRENT FILING DATE: 2001-11-08  
; PRIOR APPLICATION NUMBER: PCT/US00/12788  
; PRIOR FILING DATE: 2000-05-11  
; PRIOR APPLICATION NUMBER: US 60/134,068  
; PRIOR FILING DATE: 1999-05-13  
; NUMBER OF SEQ ID NOS: 456  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 361  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-986-480-361

Query Match 56.5%; Score 13; DB 11; Length 8;  
Best Local Similarity 25.0%; Pred. No. 6.7e+05;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
Db 1 WGLVTLAG 8

## RESULT 10

US-10-119-537-11  
; Sequence 11, Application US/10119537  
; Publication No. US20030027761A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Symonds, James Matthew  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
; FILE REFERENCE: 100086.412D1  
; CURRENT APPLICATION NUMBER: US/10/119,537  
; CURRENT FILING DATE: 2002-04-08  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 11  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Fab fragment directed against claudin cell  
; OTHER INFORMATION: adhesion recognition sequence  
US-10-119-537-11

Query Match 56.5%; Score 13; DB 15; Length 8;  
Best Local Similarity 25.0%; Pred. No. 6.7e+05;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
Db 1 WKIYSYAG 8

```

; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-231-417-485

Query Match      52.2%; Score 12; DB 12; Length 8;
Best Local Similarity 25.0%; Pred. No. 6.7e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 6;

QY      1 WXXXXXXG 8
DB      1 WLLSEKKG 8

RESULT 13
US-10-197-954-42
; Sequence 42, Application US/10197954
; Publication No. US20030119021A1
; GENERAL INFORMATION:
; APPLICANT: K'ster, Hubert
; APPLICANT: Siddiqi, Suhail
; APPLICANT: Little, Daniel
; TITLE OF INVENTION: Capture Compounds, Collections Thereof
; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: 24743-2305
; CURRENT APPLICATION NUMBER: US/10/197,954
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 60/306,019
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/314,123
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/363,433
; PRIOR FILING DATE: 2002-03-11
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-197-954-42

Query Match      47.8%; Score 11; DB 15; Length 2;
Best Local Similarity 100.0%; Pred. No. 6.7e+05; Indels 0; Gaps 0;
Matches 1; Conservative 0; Mismatches 0;

QY      1 W 1
DB      1 W 1

RESULT 14
US-09-922-261-291
; Sequence 291, Application US/09922261
; Patent No. US20020111471A1
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Puranam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/922,261
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US/09/461,697
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 485

US-08-424-550B-564
; Sequence 564, Application US/08424550B
; Publication No. US20020119447A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-NATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHROFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550B
; FILING DATE:
; CLASSIFICATION: 435435
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 564:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-424-550B-564

Query Match      52.2%; Score 12; DB 8; Length 8;
Best Local Similarity 25.0%; Pred. No. 6.7e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 6;

QY      1 WXXXXXXG 8
DB      1 WHSGLLGG 8

RESULT 12
US-10-231-417-485
; Sequence 485, Application US/10231417
; Publication No. US20030176681A1
; GENERAL INFORMATION:
; APPLICANT: Feng et al.
; TITLE OF INVENTION: 148 Human Secreted Proteins
; FILE REFERENCE: P2019P1
; CURRENT APPLICATION NUMBER: US/10/231,417
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US/09/296,622
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 619
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 485
```

; SEQ ID NO 291  
 ; LENGTH: 3  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-922-261-291

Query Match 47.8%; Score 11; DB 10; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
 Db 2 W 2

RESULT 15

US-09-922-261-405  
 ; Sequence 405, Application US/09922261  
 ; Patent No. US20020111471A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: COGENT NEUROSCIENCE, Inc.  
 ; APPLICANT: Lo, Donald C.  
 ; APPLICANT: Barney, Shawn  
 ; APPLICANT: Thomas, Mary Beth  
 ; APPLICANT: Portbury, Stuart D.  
 ; APPLICANT: Puranam, Kasturi  
 ; APPLICANT: Katz, Lawrence C.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING  
 ; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING  
 ; FILE REFERENCE: 10001-005-999  
 ; CURRENT APPLICATION NUMBER: US/09/922,261  
 ; PRIOR FILING DATE: 2001-08-03  
 ; PRIOR APPLICATION NUMBER: US/09/461,697  
 ; PRIOR FILING DATE: 1999-12-14  
 ; NUMBER OF SEQ ID NOS: 466  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 405  
 ; LENGTH: 3  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-922-261-405

Query Match 47.8%; Score 11; DB 10; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
 Db 2 W 2

Search completed: January 12, 2004, 08:34:47  
 Job time : 71 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 12, 2004, 08:19:29 ; Search time 82 Seconds

(without alignments)  
25.176 Million cell updates/sec

Title: US-09-185-908-1

Perfect score: 23

Sequence: 1 WXXXXXXG 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 452

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23:.\*  
1: sp\_archaea:.\*  
2: sp\_bacteria:.\*  
3: sp\_fungi:.\*  
4: sp\_human:.\*  
5: sp\_invertebrate:.\*  
6: sp\_mammal:.\*  
7: sp\_mhc:.\*  
8: sp\_organelle:.\*  
9: sp\_phage:.\*  
10: sp\_plant:.\*  
11: sp\_rodent:.\*  
12: sp\_virus:.\*  
13: sp\_vertebrate:.\*  
14: sp\_unclassified:.\*  
15: sp\_rvirus:.\*  
16: sp\_bacteriap:.\*  
17: sp\_archaeap:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	47.8	7	2	Q8KMS9
2	11	47.8	7	2	Q8GL04
3	11	47.8	7	2	Q8GL00
4	11	47.8	7	8	Q95945
5	11	47.8	7	10	O49223
6	11	47.8	7	15	Q8JEB1
7	11	47.8	8	2	Q85406
8	11	47.8	8	2	Q8GL21
9	11	47.8	8	2	Q8G940
10	11	47.8	8	4	Q15890
11	11	47.8	8	4	Q15888
12	11	47.8	8	4	Q8IVK3
13	11	47.8	8	5	P82685
14	11	47.8	8	5	P82686
15	11	47.8	8	5	P82687
16	11	47.8	8	5	P82688

17	11	47.8	8	5	P82689
18	11	47.8	8	6	O02831
19	11	47.8	8	6	Q95M23
20	11	47.8	8	6	Q9TRY3
21	11	47.8	8	8	Q8W8G2
22	11	47.8	8	8	Q8W8G4
23	11	47.8	8	8	Q94VC1
24	11	47.8	8	8	Q94VP6
25	11	47.8	8	8	Q8WGD7
26	11	47.8	8	8	Q94V88
27	11	47.8	8	8	Q94V82
28	11	47.8	8	8	Q9TD02
29	11	47.8	8	8	Q9T4Y2
30	11	47.8	8	8	Q94PX5
31	11	47.8	8	8	Q8W8G6
32	11	47.8	8	8	Q8W8G5
33	11	47.8	8	8	Q94VJ4
34	11	47.8	8	8	Q8W8G3
35	11	47.8	8	8	Q94V91
36	11	47.8	8	8	Q94VE4
37	11	47.8	8	8	Q94VE2
38	11	47.8	8	8	Q94VF9
39	11	47.8	8	8	Q94PX7
40	11	47.8	8	8	Q94PX6
41	11	47.8	8	8	Q94VA7
42	11	47.8	8	8	Q94VB5
43	11	47.8	8	11	Q9ET18
44	11	47.8	8	11	Q99MN0
45	11	47.8	8	11	O35835

#### ALIGNMENTS

#### RESULT 1

Q8KMS9 PRELIMINARY; PRT; 7 AA.  
AC Q8KMS9;  
DT 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)  
DE Putative transposase (Fragment).  
GN TNIA.  
OS Enterobacter sp. CH2-4.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Enterobacter.  
OX NCBI\_TaxID=143777;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-CH2-4;  
RX MEDLINE=21604134; PubMed=11763242;  
RA Mindlin S.Z., Kholodii G.Y., Gorlenko Z.M., Minakhina S.V.,  
RA Minakhin L.S., Kalyaeva E.S., Kopteva A.V., Petrova M.A.,  
RA Yurieva O.V., Nikiforov V.G.;  
RT "Mercury resistance transposons of Gram-negative environmental  
bacteria and their classification";  
RL Res. Microbiol. 152:811-822(2001).  
DR EMBL; AJ302778; CAC83058.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 966 MW; 737B1B1046DAA9A0 CRC64;

Query Match 47.8%; Score 11; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1  
Db 7 W 7

#### RESULT 2

Q8GL04 PRELIMINARY; PRT; 7 AA.  
ID Q8GL04

OS Saccharomyces cerevisiae (Baker's yeast).  
OG Mitochondrion.  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=D273-10B;  
RX MEDLINE=81069885; PubMed=6254986;  
RA Bonitz S.G., Coruzzi G., Thalenfeld B., Tzagoloff A., Macino G.;  
RT "Assembly of the mitochondrial membrane system: Structure and  
nucleotide sequence of the gene coding for subunit 1 of yeast  
cytochrome oxidase.";  
RL J. Biol. Chem. 255:11927-11941(1980).  
DR EMBL; V00694; CAA24066.1; -  
KW Mitochondrion.  
FT NON TER 1 1  
SQ SEQUENCE 7 AA; 859 MW; 75B7232362CDC460 CRC64;  
Query Match 47.8%; Score 11; DB 8; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 W 1  
DB 4 W 4  
RESULT 5  
ID O49223 PRELIMINARY; PRT; 7 AA.  
AC O49223;  
DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE HMG-1-like protein (Fragment).  
OS Glycine max (Soybean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
OX NCBI\_TaxID=3847;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Essex; TISSUE=Root;  
RX MEDLINE=91367679; PubMed=1891369;  
RA Laux T., Goldberg R.B.;  
RT "A plant DNA binding protein shares highly conserved sequence motifs  
with HMG-box proteins.";  
RL Nucleic Acids Res. 19:4769-4769(1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Essex; TISSUE=Root;  
RA Mahalingam R., Knap H.T.;  
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF047050; RAC03556.1; -  
FT NON TER 1 1  
SQ SEQUENCE 7 AA; 850 MW; 6AAAAAB378637810 CRC64;  
Query Match 47.8%; Score 11; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 W 1  
DB 2 W 2  
RESULT 6  
ID Q8JE81 PRELIMINARY; PRT; 7 AA.  
AC Q8JE81;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

OS Borrelia burgdorferi (Lyme disease spirochete).  
OG Plasmid group cp32-5.  
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.  
OX NCBI\_TaxID=139;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=93-0107;  
RA Stevenson B., Miller J.C.;  
RT "Comparative analyses of Borrelia burgdorferi erp genes and their cp32  
prophages: conservation amidst diversity.";  
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY142103; AANI7848.1; -  
KW Plasmid.  
FT NON TER 1 1  
SQ SEQUENCE 7 AA; 914 MW; 6337244330504310 CRC64;  
Query Match 47.8%; Score 11; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 W 1  
DB 1 W 1  
RESULT 3  
ID Q8GL00 PRELIMINARY; PRT; 7 AA.  
AC Q8GL00;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE PF-50 protein (Fragment).  
OS Borrelia burgdorferi (Lyme disease spirochete).  
OG Plasmid group cp32-13.  
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.  
OX NCBI\_TaxID=139;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Cal5;  
RA Stevenson B., Miller J.C.;  
RT "Comparative analyses of Borrelia burgdorferi erp genes and their cp32  
prophages: conservation amidst diversity.";  
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY142106; AANI7857.1; -  
FT NON TER 1 1  
SQ SEQUENCE 7 AA; 928 MW; 6337233050437350 CRC64;  
Query Match 47.8%; Score 11; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 W 1  
DB 2 W 2  
RESULT 4  
ID Q95945 PRELIMINARY; PRT; 7 AA.  
AC Q95945;  
DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Inside intron 5 (Fragment).

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Truncated pol protein (Fragment).  
GN POL.

OS Human immunodeficiency virus 1.  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;

RN [1]

RN SEQUENCE FROM N.A.

RC STRAIN=4874;

RX MEDLINE=22056123; PubMed=12060770;

RA Beerenwinkel N., Schmidt B., Walter H., Kaiser R., Lengauer T.,  
RA Hoffmann D., Korn K., Seibig J.;

RT "Diversity and complexity of HIV-1 drug resistance: A bioinformatics  
RT approach to predicting phenotype from genotype.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:8271-8276(2002).

DR EMBL; AF347267; AAK32344.1; -

FT NON TER

SQ SEQUENCE 7 AA; 885 MW; 76C37731A046C700 CRC64;

Query Match 47.8%; Score 11; DB 15; Length 7;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1

Db 6 W 6

RESULT 7

O85406

ID O85406 PRELIMINARY; PRT; 8 AA.

AC O85406;

DT 01-NOV-1998 (TrEMBLrel. 08, Created)

DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Hypothetical 1.0 kDa protein (Fragment).

OS Coccidia burnetii.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;

OC Coxiellaceae; Coxiella.

OX NCBI\_TaxID=777;

RN [1]

RN SEQUENCE FROM N.A.

RC STRAIN=Nine Mile Phase I;

RX MEDLINE=98348442; PubMed=9683477;

RA Williams H., Jaeger C., Baljer G.;

RT "Physical and genetic map of the obligate intracellular bacterium

RT Coccidia burnetii.";

RL J. Bacteriol. 180:3816-3822(1998).

DR EMBL; AF064963; AAD09947.1; -

KW Hypothetical protein.

FT NON TER

SQ SEQUENCE 8 AA; 993 MW; 046B5AA453772727 CRC64;

Query Match 47.8%; Score 11; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1

Db 4 W 4

RESULT 8

O8GL21

ID O8GL21 PRELIMINARY; PRT; 8 AA.

AC O8GL21;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE PP-50 protein (Fragment).

OS Borrelia burgdorferi (Lyme disease spirochete).

OG Plasmid group cp32-8.

OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.  
OX NCBI\_TaxID=139;

RN [1]

RN SEQUENCE FROM N.A.

RC STRAIN=Sh-2-82;

RA Stevenson B., Miller J.C.;

RT "Comparative analyses of Borrelia burgdorferi erp genes and their cp32  
RT prophages: conservation amidst diversity.";

RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY142094; AAN17903.1; -

KW Plasmid.

FT NON TER

SQ SEQUENCE 8 AA; 1042 MW; 1437244337204373 CRC64;

Query Match 47.8%; Score 11; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1

Db 2 W 2

RESULT 9

O8G940

ID O8G940 PRELIMINARY; PRT; 8 AA.

AC O8G940;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE PP-50 protein (Fragment).

GN PP-50.

OS Borrelia burgdorferi (Lyme disease spirochete).

OC Plasmid group cp32-9, and Plasmid group cp32-12.

OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.

OX NCBI\_TaxID=139;

RN [1]

RN SEQUENCE FROM N.A.

RC STRAIN=DNI27c13-2, and Sh-2-82;

RA Stevenson B., Miller J.C.;

RT "Comparative analyses of Borrelia burgdorferi erp genes and their cp32  
RT prophages: conservation amidst diversity.";

RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY142104; AAN17853.1; -

DR EMBL; AY142097; AAN17907.1; -

KW Plasmid.

FT NON TER

SQ SEQUENCE 8 AA; 1042 MW; 1437244330504373 CRC64;

Query Match 47.8%; Score 11; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1

Db 2 W 2

RESULT 10

Q15890

ID Q15890 PRELIMINARY; PRT; 8 AA.

AC Q15890;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE (Clone XP19C12A) (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RN SEQUENCE FROM N.A.

RC TISSUE-Placenta;  
 RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,  
 RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsey E.A., Zhao Z.-Y.,  
 RA Caskey C.T.H.;  
 RT "Isolation of chromosome-specific genes by reciprocal probing of  
 RT arrayed cDNAs and cosmid libraries."  
 RL Hum. Mol. Genet. 0:0-0(1995).  
 DR EMBL; L32083; AAA73880.1; --  
 FT NON\_TER 1 1  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 975 MW; 605EAC5BBA5A2D3 CRC64;  
 Query Match 47.8%; Score 11; DB 4; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 W 1  
 Db 1 W 1  
 RESULT 11  
 Q15888 PRELIMINARY; PRT; 8 AA.  
 ID Q15888  
 AC Q15888  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE (Clone XP15H8A) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Placenta;  
 RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,  
 RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsey E.A., Zhao Z.-Y.,  
 RA Caskey C.T.H.;  
 RT "Isolation of chromosome-specific genes by reciprocal probing of  
 RT arrayed cDNAs and cosmid libraries."  
 RL Hum. Mol. Genet. 0:0-0(1995).  
 DR EMBL; L32069; AAA73878.1; --  
 FT NON\_TER 1 1  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 1068 MW; 0315A37EAB5B0763 CRC64;  
 Query Match 47.8%; Score 11; DB 4; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 W 1  
 Db 6 W 6  
 RESULT 12  
 Q81VK3 PRELIMINARY; PRT; 8 AA.  
 ID Q81VK3  
 AC Q81VK3  
 DT 01-MAR-2003 (TREMBLrel. 23, Created)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Steerin2 (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Placenta;  
 RA Peeters P.J., Verhasselt P., Moechars D.W., Luyten W.H.M.L.,  
 RA Gysen J.J.G.H.;  
 RT "Isolation and structural elucidation of eight kinins from the  
 RT sensorineural defects in mice hypomorphic for a mammalian homolog of  
 RT unc-53.";  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases..  
 DR EMBL; AJ488208; CAD32561.1; --  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 1030 MW; E8A7245417737726 CRC64;  
 Query Match 47.8%; Score 11; DB 4; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 W 1  
 Db 3 W 3  
 RESULT 13  
 P82685 PRELIMINARY; PRT; 8 AA.  
 ID P82685  
 AC P82685  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE Kinin-1 (PEA-K-1)  
 OS Periplaneta americana (American cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
 OC Blattellidae; Periplaneta.  
 OX NCBI\_TaxID=6978;  
 RN [1]  
 RP SEQUENCE, AND FUNCTION.  
 RC TISSUE-CORPORA CARDIACA;  
 RX MEDLINE=98010462; PubMed=9350979;  
 RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;  
 RT "Isolation and structural elucidation of eight kinins from the  
 RT retrocerebral complex of the American cockroach, Periplaneta  
 americana.";  
 RL Regul. Pept. 71:199-205(1997).  
 CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
 CC (MYOTROPIC ACTIVITY).  
 CC -1- SIMILARITY: BELONGS TO THE KININ FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 8 8  
 FT SEQUENCE 8 AA; 950 MW; 326365B5449D5A774 CRC64;  
 SQ SEQUENCE 8 AA; 950 MW; 326365B5449D5A774 CRC64;  
 Query Match 47.8%; Score 11; DB 5; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 W 1  
 Db 7 W 7  
 RESULT 14  
 P82686 PRELIMINARY; PRT; 8 AA.  
 ID P82686  
 AC P82686  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE Kinin-2 (PEA-K-2).  
 OS Periplaneta americana (American cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
 OC Blattellidae; Periplaneta.  
 OX NCBI\_TaxID=6978;  
 RN [1]  
 RP SEQUENCE, AND FUNCTION.  
 RC TISSUE-CORPORA CARDIACA;  
 RX MEDLINE=98010462; PubMed=9350979;  
 RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;  
 RT "Isolation and structural elucidation of eight kinins from the

RT retrocerebral complex of the American cockroach, Periplaneta  
RT americana.";

RL Regul. Pept. 71:199-205(1997).

CC -|- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY

CC -|- (MYOTROPIC ACTIVITY).

CC -|- SIMILARITY: BELONGS TO THE KININ FAMILY.

KW Neuropeptide; Amidation.

FT MOD RES 8 8

SQ SEQUENCE 8 AA; 856 MW; DC6365A5B9D5BDDA CRC64;

Query Match

47.8%; Score 11; DB 5; Length 8;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1

DB 7 W 7

# RESULT 15

P82687

ID P82687 PRELIMINARY; PRT; 8 AA.

AC P82687;

DT 01-MAR-2001 (TREMELrel. 16, Created)

DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)

DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)

DE Kinin-3 (PEA-K-3).

OS Periplaneta americana (American cockroach).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;

OC Blattellidae; Periplaneta.

OX NCBI TaxID=6978;

RN [1]

RP SEQUENCE AND FUNCTION.

RC TISSUE=CORPORA CARDIACA;

RX MEDLINE=98010462; PubMed=9350979;

RA Fredel R., Kellner R., Rapus J., Penzlin H., Gaede G.;

RT "Isolation and structural elucidation of eight kinins from the

RT retrocerebral complex of the American cockroach, Periplaneta

RT americana.";

RL Regul. Pept. 71:199-205(1997).

CC -|- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY

CC -|- (MYOTROPIC ACTIVITY).

CC -|- SIMILARITY: BELONGS TO THE KININ FAMILY.

KW Neuropeptide; Amidation.

FT MOD RES 8 8

SQ SEQUENCE 8 AA; 909 MW; DC6365B49D5A76A CRC64;

Query Match

47.8%; Score 11; DB 5; Length 8;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1

DB 7 W 7

Search completed: January 12, 2004, 08:25:14

Job time : 85 secs

Antibody modulation of claudin-mediated cell adhesion for increasing

## ALIGNMENTS



DT 28-SEP-2000 (first entry)  
 DE Claudin-7 cyclic cell adhesion recognition sequence SEQ ID NO: 447.  
 XX  
 KW Claudin-7 modulating agent; cell adhesion recognition sequence;  
 KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
 KW graft rejection; cyclic.  
 XX  
 OS Mammalia.  
 XX  
 PN WO200026360-A1.  
 XX  
 PD 11-MAY-2000.  
 XX  
 PF 03-NOV-1999; 99WO-CA01029.  
 XX  
 PR 03-NOV-1998; 98US-0185908.  
 PR 30-MAR-1999; 99US-0282029.  
 XX  
 PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
 XX  
 XX Blaschuck OW, Symonds JM, Gour BJ;  
 FI WPI; 2000-365610/31.  
 XX  
 DR WPI; 2000-365610/31.  
 XX  
 XX Antibody modulation of claudin-mediated cell adhesion for increasing  
 PT vasopermeability, for delivering drugs to tumors and the nervous system  
 PT and across the skin -  
 PT  
 XX  
 PS Claim 79; Page 105; 121pp; English.  
 XX  
 CC The present invention relates to the use of peptides as claudin-mediated  
 CC cell adhesion modulators. The claudin-7 group of proteins are cadherins,  
 CC which are membrane glycoproteins involved in cell adhesion. In some  
 CC situations, cell adhesion occurs at abnormal levels, and these peptides  
 CC can be used to modulate these levels, and thus treat autoimmune diseases,  
 CC inflammatory diseases and cancer, and aid wound healing and implant  
 CC adhesion. In addition, they can also be used to facilitate drug delivery  
 CC to the desired target site. The present sequence has a cyclic  
 CC conformation.  
 XX  
 SQ Sequence 8 AA;  
 Query Match 60.9%; Score 14; DB 21; Length 8;  
 Best Local Similarity 25.0%; Pred. No. 9.3e+05;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 Qy 1 WXXXXXXG 8  
 Db 1 WQSSSYAG 8  
 RESULT 5  
 AAB06917  
 ID AAB06917 standard; Protein; 8 AA.  
 XX  
 AC AAB06917;  
 XX  
 DT 05-OCT-2000 (first entry)  
 XX  
 DE Claudin-7 cell adhesion recognition modulating sequence SEQ ID NO: 50.  
 KW Claudin-7 modulating agent; cell adhesion recognition sequence;  
 KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
 KW graft rejection.  
 XX  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FT Modified-site 1  
 FT Modified-site 8 /note= "N-terminal acetyl"  
 FT Modified-site 8 /note= "C-terminal amide"  
 FT

XX WO200026360-A1.  
 PN 11-MAY-2000.  
 PD 03-NOV-1999; 99WO-CA01029.  
 PF 03-NOV-1998; 98US-0185908.  
 PR 30-MAR-1999; 99US-0282029.  
 XX  
 PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
 XX  
 XX Blaschuck OW, Symonds JM, Gour BJ;  
 FI WPI; 2000-365610/31.  
 XX  
 DR WPI; 2000-365610/31.  
 XX  
 XX Antibody modulation of claudin-mediated cell adhesion for increasing  
 PT vasopermeability, for delivering drugs to tumors and the nervous system  
 PT and across the skin -  
 PT  
 XX  
 PS Claim 77; Page 104; 121pp; English.  
 XX  
 CC The present sequence is a peptide which can be used in a claudin-mediated  
 CC cell adhesion modulator. The claudin group of proteins are cadherins,  
 CC which are membrane glycoproteins involved in cell adhesion. In some  
 CC situations, cell adhesion occurs at abnormal levels, and this peptide  
 CC can be used to modulate these levels, and thus treat autoimmune diseases,  
 CC inflammatory diseases and cancer, and aid wound healing and implant  
 CC adhesion. In addition, it can also be used to facilitate drug delivery  
 CC to the desired target site.  
 XX  
 SQ Sequence 8 AA;  
 Query Match 60.9%; Score 14; DB 21; Length 8;  
 Best Local Similarity 25.0%; Pred. No. 9.3e+05;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 Qy 1 WXXXXXXG 8  
 Db 1 WQSSSYAG 8  
 RESULT 6  
 AAB56267  
 ID AAB56267 standard; Protein; 8 AA.  
 XX  
 AC AAB56267;  
 XX  
 DT 13-MAR-2001 (first entry)  
 XX  
 DE Human secreted protein sequence encoded by gene 65 SEQ ID NO:361.  
 XX  
 KW Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;  
 KW antirheumatic; antiproliferative; cytostatic; cardiac; vasotropic;  
 KW cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide;  
 KW fungicide; ophthalmological; gene therapy; pathological condition;  
 KW autoimmune disease; rheumatoid arthritis; hyperproliferative disorder;  
 KW neoplasia; cardiovascular disorder; cardiac arrest; cerebral ischaemia;  
 KW cerebrovascular disorder; angiogenesis; nervous system disorder;  
 KW Alzheimer's disease; infection; ocular disorder; corneal infection;  
 KW wound healing; skin aging; food additive; preservative.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200070042-A1.  
 XX  
 PD 23-NOV-2000.  
 XX  
 PF 11-MAY-2000; 2000WO-US12788.  
 XX  
 PR 13-MAY-1999; 99US-0134068.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.

XX Roen CA, Ruben SM, Moore PA, Young PE, Komatsoulis GA, Birse CB;  
PI Duan RD, Florence KA, Soppet DR;  
XX WPI; 2000-679828/66.  
XX Isolated nucleic acid molecule encoding a human secreted protein is  
PT used in preventing, treating or ameliorating a medical condition -  
XX Disclosure; Page 1021; 1065pp; English.  
XX The polynucleotide sequences given in AAC99818 to AAC99977 encode the  
CC human secreted proteins given in AAB56077 to AAB56362. Human secreted  
CC proteins have activities based on the tissues and cells the genes are  
CC expressed in. Examples of activities include: immunosuppressive;  
CC antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant;  
CC vasotropic; cerebroprotective; neurotropic; neuroprotective; antibacterial;  
CC virucide; fungicide; and ophthalmological. The human secreted  
CC polynucleotides and proteins can be used to prevent, treat or ameliorate  
CC a medical condition in e.g. humans, mice, rabbits, goats, horses, cats,  
CC dogs, chickens or sheep. They are also used in diagnosing a pathological  
CC condition or susceptibility to a pathological condition. Disorders which  
CC are diagnosed or treated include autoimmune diseases e.g. rheumatoid  
CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or  
CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular  
CC disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders  
CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and  
CC fungi and ocular disorders e.g. corneal infection. The proteins can also  
CC be used to aid wound healing and epithelial cell proliferation, to  
CC prevent skin aging due to sunburn, to maintain organs before  
CC transplantation, for supporting cell culture of primary tissues, to  
CC regenerate tissues and in chemotaxis. The proteins can also be used as a  
CC food additive or preservative to increase or decrease storage  
CC capabilities. AAC99809 to AAC99817 and AAB56076 represent sequences used  
CC in the exemplification of the present invention.  
XX Sequence 8 AA;  
SQ  
Query Match 56.5%; Score 13; DB 21; Length 8;  
Best Local Similarity 25.0%; Pred. No. 9.3e+05;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Oy 1 WXXXXXXG 8  
Db 1 WGLVTLAG 8  
RESULT 7  
AAB06419  
ID AAB06419 standard; peptide; 8 AA.  
XX AAB06419;  
XX 28-SEP-2000 (first entry)  
XX Claudin-1 cell adhesion recognition sequence SEQ ID NO: 34.  
XX Claudin-1 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection.  
XX Mammalia.  
XX WO200026360-A1.  
XX 11-MAY-2000.  
XX 03-NOV-1999; 99WO-CA01029.  
XX 03-NOV-1998; 98US-0185908.  
XX 30-MAR-1999; 99US-0282029.  
XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
PA

XX Blaschuck OW, Symonds JM, Gour BJ;  
XX WPI; 2000-365610/31.  
XX Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX Claim 39; Page 96; 121pp; English.  
XX The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site.  
XX Sequence 8 AA;  
SQ  
Query Match 56.5%; Score 13; DB 21; Length 8;  
Best Local Similarity 25.0%; Pred. No. 9.3e+05;  
Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Oy 1 WXXXXXXG 8  
Db 1 WKIYSYAG 8  
RESULT 8  
AAB06426  
ID AAB06426 standard; peptide; 8 AA.  
XX AAB06426;  
XX 28-SEP-2000 (first entry)  
XX Claudin-1 cell adhesion recognition sequence SEQ ID NO: 485.  
XX Claudin-1 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection.  
XX Mammalia.  
XX WO200026360-A1.  
XX 11-MAY-2000.  
XX 03-NOV-1999; 99WO-CA01029.  
XX 03-NOV-1998; 98US-0185908.  
XX 30-MAR-1999; 99US-0282029.  
XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX Blaschuck OW, Symonds JM, Gour BJ;  
XX WPI; 2000-365610/31.  
XX Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX Claim 39; Page 96; 121pp; English.  
XX The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC

CC inflammatory diseases and cancer, and aid wound healing and implant  
 CC adhesion. In addition, they can also be used to facilitate drug delivery  
 CC to the desired target site.

XX Sequence 8 AA;

Query Match 56.5%; Score 13; DB 21; Length 8;  
 Best Local Similarity 25.0%; Pred. No. 9.3e+05;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
 |  
 Db 1 WRIYSYAG 8

RESULT 9

AAB06479  
 ID AAB06479 standard; peptide; 8 AA.

XX AC

XX AC AAB06479;

XX DT 28-SEP-2000 (first entry)

XX DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 110.

XX KW Claudin-1 modulating agent; cell adhesion recognition sequence;  
 KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
 KW graft rejection; cyclic.

XX OS Mammalia.

XX PN WO200026360-A1.

XX PD 11-MAY-2000.

XX PF 03-NOV-1999; 99WO-CA01029.

XX PR 03-NOV-1998; 98US-0185908.

XX PR 30-MAR-1999; 99US-0282029.

XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.

XX PI Blaschuck OW, Symonds JM, Gour BJ;

XX DR WPI; 2000-365610/31.

XX PT Antibody modulation of claudin-mediated cell adhesion for increasing  
 PT vasopermeability, for delivering drugs to tumors and the nervous system  
 PT and across the skin -

XX PS Claim 43; Page 97; 121pp; English.

XX CC The present invention relates to the use of peptides as claudin-mediated  
 CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,  
 CC which are membrane glycoproteins involved in cell adhesion. In some  
 CC situations, cell adhesion occurs at abnormal levels, and these peptides  
 CC can be used to modulate these levels, and thus treat autoimmune diseases,  
 CC inflammatory diseases and cancer, and aid wound healing and implant  
 CC adhesion. In addition, they can also be used to facilitate drug delivery  
 CC to the desired target site. The present sequence has a cyclic  
 CC conformation.

XX SQ Sequence 8 AA;

Query Match 56.5%; Score 13; DB 21; Length 8;  
 Best Local Similarity 25.0%; Pred. No. 9.3e+05;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
 |  
 Db 1 WKIYSYAG 8

RESULT 10

AAB06512

ID AAB06512 standard; peptide; 8 AA.

XX AC AAB06512;

XX DT 28-SEP-2000 (first entry)

XX DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 519.

XX KW Claudin-1 modulating agent; cell adhesion recognition sequence;  
 KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
 KW graft rejection; cyclic.

XX OS Mammalia.

XX PN WO200026360-A1.

XX PD 11-MAY-2000.

XX PF 03-NOV-1999; 99WO-CA01029.

XX PR 03-NOV-1998; 98US-0185908.

XX PR 30-MAR-1999; 99US-0282029.

XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.

XX PI Blaschuck OW, Symonds JM, Gour BJ;

XX DR WPI; 2000-365610/31.

XX PT Antibody modulation of claudin-mediated cell adhesion for increasing  
 PT vasopermeability, for delivering drugs to tumors and the nervous system  
 PT and across the skin -

XX PS Claim 43; Page 97; 121pp; English.

XX CC The present invention relates to the use of peptides as claudin-mediated  
 CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,  
 CC which are membrane glycoproteins involved in cell adhesion. In some  
 CC situations, cell adhesion occurs at abnormal levels, and these peptides  
 CC can be used to modulate these levels, and thus treat autoimmune diseases,  
 CC inflammatory diseases and cancer, and aid wound healing and implant  
 CC adhesion. In addition, they can also be used to facilitate drug delivery  
 CC to the desired target site. The present sequence has a cyclic  
 CC conformation.

XX SQ Sequence 8 AA;

Query Match 56.5%; Score 13; DB 21; Length 8;  
 Best Local Similarity 25.0%; Pred. No. 9.3e+05;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WXXXXXXG 8  
 |  
 Db 1 WRIYSYAG 8

RESULT 11

AAB06583

ID AAB06583 standard; peptide; 8 AA.

XX AC AAB06583;

XX DT 28-SEP-2000 (first entry)

XX DE Claudin-3 cell adhesion recognition sequence SEQ ID NO: 58.

XX KW Claudin-3 modulating agent; cell adhesion recognition sequence;  
 KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
 KW graft rejection.

XX OS Mammalia.



SQ Sequence 8 AA;

Query Match 56.5%; Score 13; DB 21; Length 8;  
 Best Local Similarity 25.0%; Pred. No. 9.3e+05;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 WXXXXXXG 8  
 |  
 Db 1 WRVTAFIG 8

## RESULT 14

AAB06698  
 ID AAB06698 standard; peptide; 8 AA.

XX  
 AC AAB06698;

DT 28-SEP-2000 (first entry)

XX Claudin-4 cyclic cell adhesion recognition sequence SEQ ID NO: 216.

XX Claudin-4 modulating agent; cell adhesion recognition sequence;  
 KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
 KW graft rejection; cyclic.

XX Mammalia.

XX WO200026360-A1.

XX 11-MAY-2000.

XX 03-NOV-1999; 99WO-CA01029.

XX 03-NOV-1998; 98US-0185908.

XX 30-MAR-1999; 99US-0282029.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuck OW, Symonds JM, Gour BJ;

XX WPI; 2000-365610/31.

XX Antibody modulation of claudin-mediated cell adhesion for increasing  
 PT vasopermeability, for delivering drugs to tumors and the nervous system  
 PT and across the skin -

XX Claim 61; Page 101; 121pp; English.

XX The present invention relates to the use of peptides as claudin-mediated  
 CC cell adhesion modulators. The claudin-4 group of proteins are cadherins,  
 CC which are membrane glycoproteins involved in cell adhesion. In some  
 CC situations, cell adhesion occurs at abnormal levels, and these peptides  
 CC can be used to modulate these levels, and thus treat autoimmune diseases,  
 CC inflammatory diseases and cancer, and aid wound healing and implant  
 CC adhesion. In addition, they can also be used to facilitate drug delivery  
 CC to the desired target site. The present sequence has a cyclic  
 CC conformation.

SQ Sequence 8 AA;

Query Match 56.5%; Score 13; DB 21; Length 8;  
 Best Local Similarity 25.0%; Pred. No. 9.3e+05;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 WXXXXXXG 8  
 |  
 Db 1 WRVTAFIG 8

## RESULT 15

AAB06764  
 ID AAB06764 standard; peptide; 8 AA.

XX

AC AAB06764;

XX 28-SEP-2000. (first entry)

XX Claudin-6/9 cell adhesion recognition sequence SEQ ID NO: 335.

XX Claudin-6 modulating agent; claudin-9 modulating agent;  
 KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;  
 KW inflammatory disease; cancer; graft rejection.

XX Mammalia.

XX WO200026360-A1.

XX 11-MAY-2000.

XX 03-NOV-1999; 99WO-CA01029.

XX 03-NOV-1998; 98US-0185908.

XX 30-MAR-1999; 99US-0282029.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuck OW, Symonds JM, Gour BJ;

XX WPI; 2000-365610/31.

XX Antibody modulation of claudin-mediated cell adhesion for increasing  
 PT vasopermeability, for delivering drugs to tumors and the nervous system  
 PT and across the skin -

XX Claim 70; Page 103; 121pp; English.

XX The present invention relates to the use of peptides as claudin-mediated  
 CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins  
 CC are cadherins, which are membrane glycoproteins involved in cell  
 CC adhesion. In some situations, cell adhesion occurs at abnormal levels,  
 CC and these peptides can be used to modulate these levels, and thus treat  
 CC autoimmune diseases, inflammatory diseases and cancer, and aid wound  
 CC healing and implant adhesion. In addition, they can also be used to  
 CC facilitate drug delivery to the desired target site.

SQ Sequence 8 AA;

Query Match 56.5%; Score 13; DB 21; Length 8;  
 Best Local Similarity 25.0%; Pred. No. 9.3e+05;  
 Matches 2; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 WXXXXXXG 8  
 |  
 Db 1 WKVTAFIG 8

Search completed: January 12, 2004, 08:22:58  
 Job time : 74 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 12, 2004, 08:20:13 ; Search time 37 Seconds  
(without alignments)  
20.793 Million cell updates/sec

Title: US-09-185-908-1  
Perfect score: 23  
Sequence: 1 WXXXXXXG 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 604

Minimum DB seq length: 0  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	47.8	3	3 F37196	bradykinin-potenti
2	11	47.8	4	2 A34626	RPCH-related neuro
3	11	47.8	4	2 B53284	T-cell receptor be
4	11	47.8	4	2 PT0661	T-cell receptor be
5	11	47.8	5	2 A32516	cholecystokinin-5
6	11	47.8	5	2 A60803	neuropeptide - sea
7	11	47.8	5	2 JH0253	gut pentapeptide -
8	11	47.8	5	2 G37196	bradykinin-potenti
9	11	47.8	5	2 PT0281	ig heavy chain CRD
10	11	47.8	5	2 PT0308	ig heavy chain CRD
11	11	47.8	5	2 PT0729	T-cell receptor be
12	11	47.8	5	2 PT0580	T-cell receptor be
13	11	47.8	6	2 S66195	alcohol dehydrogen
14	11	47.8	6	2 B34835	dnaa protein - fee
15	11	47.8	6	2 A32633	dihydrofolate redu
16	11	47.8	6	2 B31263	dihydrofolate redu
17	11	47.8	6	2 A61068	locustakinin - mig
18	11	47.8	6	2 B35640	cerebellar degener
19	11	47.8	6	2 PT0629	T-cell receptor be
20	11	47.8	6	2 PT0532	T-cell receptor be
21	11	47.8	6	2 PT0519	T-cell receptor be
22	11	47.8	6	2 PT0637	T-cell receptor be
23	11	47.8	6	2 PT0641	T-cell receptor be
24	11	47.8	6	2 PT0726	T-cell receptor be
25	11	47.8	6	2 P41945	T-cell receptor ga
26	11	47.8	6	2 PT0028	pev-kinin 2 - pena
27	11	47.8	6	4 I79564	hypothetical TCL3
28	11	47.8	7	2 S21230	dermorphin (Trp-4,
29	11	47.8	7	2 A58512	venom heptapeptide

30	11	47.8	7	2 A61081	tryptophyllin, bas
31	11	47.8	7	2 S57274	triacylglycerol li
32	11	47.8	7	2 S09652	hypothetical prote
33	11	47.8	7	2 P00727	H2 class I protein
34	11	47.8	7	2 S33244	neuromodulatory pe
35	11	47.8	7	2 S33245	neuromodulatory pe
36	11	47.8	7	2 S33246	neuromodulatory pe
37	11	47.8	7	2 E48394	glycoprotein compo
38	11	47.8	7	2 PH1602	ig H chain V-D-J r
39	11	47.8	7	2 PT0526	T-cell receptor be
40	11	47.8	7	2 PT0628	T-cell receptor be
41	11	47.8	7	2 PT0642	T-cell receptor be
42	11	47.8	7	2 PT0722	T-cell receptor be
43	11	47.8	7	2 PT0688	T-cell receptor be
44	11	47.8	7	2 PT0586	T-cell receptor be
45	11	47.8	7	2 PT0728	T-cell receptor be

## ALIGNMENTS

### RESULT 1

F37196  
bradykinin-potentiating peptide 6 - island jararaca  
C:Species: Bothrops insularis (island jararaca)  
C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
R:Accession: F37196  
R:Cintrra, A.C.O.; Vieira, C.A.; Giglio, J.R.  
J. Protein Chem. 9, 221-227, 1990  
A:Title: Primary structure and biological activity of bradykinin potentiating peptide:  
A:Reference number: A37196; MUID:90351557; PMID:2386615  
A:Accession: F37196  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-3 <GIN>  
C:Keywords: pyroglutamic acid  
F:1/Modified site: pyroglutamic acid (Gln) #status experimental

Query Match 47.8%; Score 11; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
Db 3 W 3

### RESULT 2

A34626  
RPCH-related neuropeptide - ferruginous spindle  
C:Species: Fusinus ferrugineus (ferruginous spindle)  
C:Date: 06-Jul-1990 #sequence\_revision 06-Jul-1990 #text\_change 31-Dec-1993  
R:Accession: A34626  
R:Kuroki, Y.; Kanda, T.; Kubota, I.; Fujisawa, Y.; Ikeda, T.; Miura, A.; Minamitake, Y.  
Biochem. Biophys. Res. Commun. 167, 273-279, 1990  
A:Title: A molluscan neuropeptide related to the crustacean hormone, RPCH.  
A:Reference number: A34626; MUID:90179762; PMID:2310394  
A:Accession: A34626  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-4 <KUR>  
C:Keywords: neuropeptide

Query Match 47.8%; Score 11; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
Db 4 W 4

### RESULT 3

B53284  
T-cell receptor beta 2 chain D region, Dbeta2 - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999  
C:Accession: B53284  
R:Harindranath, N.; Alexander, C.B.; Mage, R.G.  
Mol. Immunol. 28, 881-888, 1991  
A:Title: Evolutionarily conserved organization and sequences of germline diversity and J  
A:Reference number: A53284; MUID:91342695; PMID:1678859  
A:Accession: B53284  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-4 <HAR>  
A:Cross-references: GB:S60737; NID:g233916; PIDN:AA819518.1; PID:g233918  
A>Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60738)  
C:Keywords: T-cell receptor

Query Match 47.8%; Score 11; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
Db 2 W 2

RESULT 4  
PT0661  
T-cell receptor beta chain V-D-J region (121-18V) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0661  
R:Peeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601; PMID:1711558  
A:Accession: PT0661  
A>Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-4 <FES>  
A:Experimental source: day 4 postnatal thymus, strain BALB/c  
C:Keywords: T-cell receptor

Query Match 47.8%; Score 11; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
Db 3 W 3

RESULT 5  
A32516  
cholecystokinin-5 - dog  
N:Alternate names: CCK-5  
C:Species: Canis lupus familiaris (dog)  
C:Date: 18-Oct-1989 #sequence\_revision 18-Oct-1989 #text\_change 18-Aug-2000  
C:Accession: A32516  
R:Shively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J.H.  
Am. J. Physiol. 252, G272-G275, 1987  
A:Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and intest  
A:Reference number: A32516; MUID:87153871; PMID:3826354  
A:Accession: A32516  
A:Molecule type: protein  
A:Residues: 1-5 <SHI>  
C:Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecysto  
C:Superfamily: Gastrin  
C:Keywords: amidated carboxyl end; neuropeptide  
P;5/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 47.8%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
Db 2 W 2

RESULT 6  
A60803  
neuropeptide - sea anemone (Anthopleura elegantissima)  
C:Species: Anthopleura elegantissima  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C:Accession: A60803  
R:Graff, D.; Grimmelikhuijzen, C.J.P.  
Brain Res. 442, 354-358, 1988  
A:Title: Isolation of <Glu-Ser-Lu-Arg-Trp-NH-2, a novel neuropeptide from sea anemone  
A:Reference number: A60803; MUID:88222764; PMID:2897223  
A:Accession: A60803  
A:Molecule type: protein  
A:Residues: 1-5 <GRA>  
C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid  
P;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
P;5/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 47.8%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
Db 5 W 5

RESULT 7  
JH0253  
gut pentapeptide - Japanese eel  
C:Species: Anguilla japonica (Japanese eel)  
C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 11-Apr-1995  
C:Accession: JH0253  
R:Uesaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.  
Biochem. Biophys. Res. Commun. 180, 828-832, 1991  
A:Title: Structure and function of a pentapeptide isolated from the gut of the eel.  
A:Reference number: JH0253; MUID:92062113; PMID:1953755  
A:Accession: JH0253  
A:Molecule type: protein  
A:Residues: 1-5 <UES>  
A:Experimental source: gut  
C:Comment: This peptide increased basal tone of the circular muscle of the esophagoga  
, and of the circular muscle of the gastro-intestinal junction.

Query Match 47.8%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
Db 3 W 3

RESULT 8  
G37196  
bradykinin-potentiating peptide 7 - island jamaraca  
C:Species: Bothrops insularis (island jamaraca)  
C:Date: 14-Feb-1992 #sequence\_revision 01-Dec-1992 #text\_change 05-Aug-1994  
C:Accession: G37196  
R:Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.  
J. Protein Chem. 9, 221-227, 1990  
A:Title: Primary structure and biological activity of bradykinin potentiating peptide  
A:Reference number: A37196; MUID:90351557; PMID:2386615  
A:Accession: G37196  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-5 <CIN>

C;Keywords: pyroglutamic acid  
F1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 47.8%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
|  
Db 3 W 3

## RESULT 9

PT0281 Ig heavy chain CRD3 region (clone 4-91C) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C;Accession: PT0281

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J

A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0281

A;Molecule type: DNA

A;Residues: 1-5 <YAM>

A;Experimental source: B lymphocyte

C;Keywords: heterotetramer; immunoglobulin

Query Match 47.8%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
|  
Db 4 W 4

## RESULT 10

PT0308

Ig heavy chain CRD3 region (clone 6-88) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C;Accession: PT0308

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J

A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0308

A;Molecule type: DNA

A;Residues: 1-5 <YAM>

A;Experimental source: B lymphocyte

C;Keywords: heterotetramer; immunoglobulin

Query Match 47.8%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
|  
Db 2 W 2

## RESULT 11

PT0729

T-cell receptor beta chain V-D-J region (120-1J) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C;Accession: PT0640; PT0685; PT0729

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0640

A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-5 <FE2>  
A;Experimental source: newborn thymus, strain BALB/c, clone 120-1J  
A;Accession: PT0685  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-5 <FE2>  
A;Experimental source: day 18 fetal thymus, strain BALB/c, clone 154-1C  
A;Accession: PT0729  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-5 <PE3>  
A;Experimental source: newborn thymus, strain BALB/c, clone 135-1AG  
C;Keywords: T-cell receptor

Query Match 47.8%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
|  
Db 5 W 5

## RESULT 12

PT0580

T-cell receptor beta chain V-D-J region (159-2B) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C;Accession: PT0580

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0580

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-5 <FE2>

A;Experimental source: day 19 fetal thymus, strain BALB/c

C;Keywords: T-cell receptor

## Query Match

47.8%; Score 11; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
|  
Db 4 W 4

## RESULT 13

S66195

alcohol dehydrogenase (EC 1.1.1.1) class III low affinity form - cod (Gadus sp.) (frag

C;Species: Gadus sp. (cod)

C;Date: 19-Mar-1997 #sequence\_revision 29-Aug-1997 #text\_change 12-Jun-1998

C;Accession: S66195

R;Hjeltnes, L.; Hackett, M.; Shafiqat, J.; Danielsson, O.; Iida, J.; Hendrickson, R.C.

FEBS Lett. 367, 237-240, 1995

A;Title: Multiplicity of N-terminal structures of medium-chain alcohol dehydrogenases.

A;Reference number: S66191; MUID:95331382; PMID:7607314

A;Accession: S66195

A;Molecule type: protein

A;Residues: 1-6 <HJE>

C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology

C;Keywords: alcohol metabolism; NAD; oxidoreductase

## Query Match

47.8%; Score 11; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1

```

Db      |
      5 W 5

RESULT 14
B34835
dnaA protein - Pseudomonas aeruginosa (fragment)
C;Species: Pseudomonas aeruginosa
C;Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 08-Oct-1999
C;Accession: B34835
R;Yee, T.W.; Smith, D.W.
Proc. Natl. Acad. Sci. U.S.A. 87, 1278-1282, 1990
A;Title: Pseudomonas chromosomal replication origins: a bacterial class distinct from Es
A;Reference number: A34835; MUID:90160310; PMID:2106132
A;Accession: B34835
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-6 <YEE>
A;Cross-references: GB:M30125; NID:g151419; PIDN:AAA25916.1; PID:g151421
C;Keywords: DNA binding

Query Match      47.8%; Score 11; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 W 1
      |
Db      6 W 6

RESULT 15
A31263
dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodium f
C;Species: Plasmodium falciparum
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996
C;Accession: A31263
R;Peterson, D.S.; Walliker, D.; Welles, T.E.
Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988
A;Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate synthase
A;Reference number: A94217; MUID:89057886; PMID:2904149
A;Accession: A31263
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-6 <PET>
C;Keywords: methyltransferase; NADP; oxidoreductase

Query Match      47.8%; Score 11; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 W 1
      |
Db      3 W 3

Search completed: January 12, 2004, 08:26:05
Job time : 39 secs

```

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 12, 2004, 08:13:32 ; Search time 23 seconds  
(without alignments)  
16.357 Million cell updates/sec

Title: US-09-185-908-1  
Perfect score: 23  
Sequence: 1 WXXXXXXG 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 158

Minimum DB seq length: 0  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	11	47.8	4	1 OCP3 OCTMI	P58649 octopus min
2	11	47.8	5	1 BPP7 BOTIN	P30425 bothrops in
3	11	47.8	5	1 UF01 MOUSE	P38639 mus musculus
4	11	47.8	6	1 E101 LITRU	P82096 litoria rub
5	11	47.8	6	1 LOK1 LOCMI	P41491 locusta mig
6	11	47.8	7	1 BRHP CONTM	P58803 conus imper
7	11	47.8	7	1 TPY1 PACDA	P83455 pachymedusa
8	11	47.8	7	1 TY51 LITRU	P82065 litoria rub
9	11	47.8	7	1 WWA1 ACHFU	P35919 achatina fu
10	11	47.8	7	1 WWA2 ACHFU	P35920 achatina fu
11	11	47.8	7	1 WWA3 ACHFU	P35921 achatina fu
12	11	47.8	8	1 AC1 THUAL	P18691 thunnus alb
13	11	47.8	8	1 AKHG GRYBI	P14086 gryllus bim
14	11	47.8	8	1 AKH LIBAU	P25418 libellula a
15	11	47.8	8	1 AKH MELML	P25423 melolontha
16	11	47.8	8	1 AKH TABAT	P14595 tabanus atr
17	11	47.8	8	1 CCKN MACEU	P30369 macropus eu
18	11	47.8	8	1 CMW2 CONPU	P58785 conus purpu
19	11	47.8	8	1 HTP1 PERAM	P04548 periplaneta
20	11	47.8	8	1 HTP2 PERAM	P04549 periplaneta
21	11	47.8	8	1 HTP TENMO	P25419 tenebrio mo
22	11	47.8	8	1 LCK1 LEUMA	P21140 leucophaea
23	11	47.8	8	1 LCK2 LEUMA	P21141 leucophaea
24	11	47.8	8	1 LCK3 LEUMA	P21142 leucophaea
25	11	47.8	8	1 LCK4 LEUMA	P21143 leucophaea
26	11	47.8	8	1 LCK5 LEUMA	P19987 leucophaea
27	11	47.8	8	1 LCK6 LEUMA	P19988 leucophaea
28	11	47.8	8	1 LCK7 LEUMA	P19989 leucophaea
29	11	47.8	8	1 LCK8 LEUMA	P19990 leucophaea
30	11	47.8	8	1 PLP BRANA	P81707 brassica bo
31	11	47.8	8	1 RPCH PANBO	P08939 pandalus no
32	11	47.8	8	1 RT34 BOVIN	P82929 bos taurus
33	6	26.1	3	1 GRWM HUMAN	P01157 homo sapien

34	6	26.1	4	1 ACH1 ACHFU	P35904 achatina fu
35	6	26.1	4	1 DCML PSECH	P19916 pseudomonas
36	6	26.1	4	1 E0S1 HUMAN	P02731 homo sapien
37	6	26.1	4	1 OCP1 OCTMI	P58648 octopus min
38	6	26.1	5	1 AL14 CARMA	P81817 cardinus ma
39	6	26.1	5	1 PAP2 PARMA	P81864 pardachirus
40	6	26.1	5	1 RE32 LITRU	P82073 litoria rub
41	6	26.1	5	1 TPIS CANPA	P54714 canis famill
42	6	26.1	5	1 UXA4 CHLTR	P38005 chlamydia t
43	6	26.1	6	1 CIP1 MYTED	P13736 mytilus edu
44	6	26.1	6	1 CIP2 MYTED	P13737 mytilus edu
45	6	26.1	6	1 PARP MONEX	P41966 moniezia ex

ALIGNMENTS

RESULT 1					
OCP3 OCTMI		STANDARD;	PRT;	4 AA.	
AC P58649,					
DT 28-FEB-2003 (Rel. 41, Created)					
DT 28-FEB-2003 (Rel. 41, Last sequence update)					
DE 28-FEB-2003 (Rel. 41, Last annotation update)					
DE Cardioactive peptides Ocp-3/Ocp-4.					
OS Octopus minor (Octopus)					
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;					
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.					
OX NCBI_TaxID=89766;					
RN [1]					
RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.					
RC TISSUE=Brain;					
RX MEDLINE=20336815; PubMed=10876044;					
RA Iwakoshi E., Hisada M., Minakata H.;					
RT "Cardioactive peptides isolated from the brain of a Japanese octopus,					
RT Octopus minor.";					
RL Peptides 21:623-630(2000).					
CC -!- FUNCTION: Cardioactive; has both positive chronotropic and					
CC inotropic effects on the heart. Ocp-4 is a 1000 time less					
CC active than Ocp-3.					
CC -!- SUBCELLULAR LOCATION: Secreted.					
CC -!- PTM: Ocp-4 has D-Ser instead of L-Ser.					
CC -!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.					
KW Hormones; D-amino acid.					
FT MOD RES 2					
SQ SEQUENCE 4 AA; 463 MW; 6AB365B810000000 CRC64;					
Query Match 47.8%; Score 11; DB 1; Length 4;					
Best Local Similarity 100.0%; Pred. No. 1.3e+05;					
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
OY 1 W 1					
Db 3 W 3					
RESULT 2					
BPP7 BOTIN		STANDARD;	PRT;	5 AA.	
ID BPP7 BOTIN					
AC P30425;					
DT 01-APR-1993 (Rel. 25, Created)					
DT 01-FEB-1994 (Rel. 28, Last sequence update)					
DT 28-FEB-2003 (Rel. 41, Last annotation update)					
DE Bradykinin-potentiating peptide S5,2 (5A) (Angiotensin-converting					
DE enzyme inhibitor).					
OS Bothrops insularis (Island jararaca) (Queimada jararaca).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;					
OC Viperidae; Crotalinae; Bothrops.					
RN NCBI_TaxID=8723;					
RN [1]					
RP SEQUENCE.					
RC TISSUE=Venom;					

RX MEDLINE=90351557; PubMed=2386615;  
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
RT "Primary structure and biological activity of bradykinin potentiating  
peptides from Bothrops insularis snake venom.";  
RL J. Protein Chem. 9:221-227(1990).  
CC -!- FUNCTION: This peptide both inhibits the activity of the  
angiotensin-converting enzyme and enhances the action of  
bradykinin by inhibiting the kinases that inactivate it.  
CC It acts as an indirect hypotensive agent.  
DR PIR; G37196; G37196.  
KW Hypotensive agent; Pyrrolidone carboxylic acid.  
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
SQ SEQUENCE 5 AA; 629 MW; 776DC37326B00000 CRC64;  
  
Query Match 47.8%; Score 11; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 W 1  
DB 3 W 3  
  
RESULT 3  
UF01\_MOUSE STANDARD; PRT; 5 AA.  
AC P38639;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 01-FEB-1995 (Rel. 31, Last annotation update)  
DE Unknown protein from 2D-page of fibroblasts (P19) (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE  
RC TISSUE=Fibroblast;  
RX MEDLINE=9500907; PubMed=7523108;  
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;  
RT "Separation and sequencing of familial and novel murine proteins  
using preparative two-dimensional gel electrophoresis.";  
RL Electrophoresis 15:735-745(1994).  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
PROTEIN IS: 6.6, ITS MW IS: 19 KDa.  
FT NON TER 5 5  
SQ SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;  
  
Query Match 47.8%; Score 11; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 W 1  
DB 1 W 1  
  
RESULT 4  
E101\_LITRU STANDARD; PRT; 6 AA.  
AC P82036;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Electrin 1.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE  
RC TISSUE=Skin secretion;

RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
RT "Peptides from the skin glands of the Australian buzzing tree frog  
Litoria electrica. Comparison with the skin peptides from Litoria  
rubella.";  
RL Aust. J. Chem. 52:639-645(1999).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
KW Amphibian defense peptide; Amidation.  
FT MOD RES 6 6 AMIDATION.  
SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;  
  
Query Match 47.8%; Score 11; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 W 1  
DB 5 W 5  
  
RESULT 5  
LOK1\_LOCMI STANDARD; PRT; 6 AA.  
ID LOK1\_LOCMI  
AC P41491;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Locustakinin I.  
OS Locusta migratoria (Migratory locust).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
OX NCBI\_TaxID=7004;  
RN [1]  
RP SEQUENCE  
RC TISSUE=Corpora cardiaca;  
RX MEDLINE=92262851; PubMed=1585017;  
RA Schoofs L., Holman G.M., Proost P., van Damme J., Hayes T.K.,  
de Loof A.;  
RT "Locustakinin, a novel myotropic peptide from Locusta migratoria,  
isolation, primary structure and synthesis.";  
RL Regul. Pept. 37:49-57(1992).  
CC -!- FUNCTION: Myotropic peptide. May be important in the stimulation  
of ion transport and inhibition of diuretic activity in Malpighian  
tubules.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
DR PIR; A61068; A61068.  
KW Neuropeptide; Amidation.  
FT MOD RES 6 6 AMIDATION.  
SQ SEQUENCE 6 AA; 654 MW; 686365A5B9CDB000 CRC64;  
  
Query Match 47.8%; Score 11; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 W 1  
DB 5 W 5  
  
RESULT 6  
BRHP\_CONIM STANDARD; PRT; 7 AA.  
ID BRHP\_CONIM  
AC P58803;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bromheptapeptide Im.  
OS Conus imperialis (Imperial cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
OX NCBI\_TaxID=35631;

RN SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
 RP TISSUE=Venom;  
 RC MEDLINE=97184108; PubMed=9030520;  
 RA Craig A.G., Jimenez E.C., Dykert J., Nielsen D.B., Gulyas J.,  
 RA Abogadie F.C., Porter J., Rivier J.E., Cruz L.J., Olivera B.M.,  
 RA McIntosh J.M.;  
 RT "A novel post-translational modification involving bromination of  
 RT tryptophan. Identification of the residue, L-6-bromotryptophan, in  
 RT peptides from *Conus imperialis* and *Conus radiatus* venom.";  
 RL J. Biol. Chem. 272:4689-4698(1997).  
 CC -1- FUNCTION: Does not elicit gross behavioral symptoms when injected  
 CC centrally or peripherally in mice.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -1- MASS SPECTROMETRY: MW=853.19; METHOD=LSIMS.  
 DR PIR: A58512; A58512;  
 KW Bromination; Amidation; Pyrrolidone carboxylic acid.  
 FT DISULFID 2 7  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 6 6 BROMINATION.  
 FT MOD\_RES 7 7 AMIDATION.  
 SQ SEQUENCE 7 AA; 795 MW; 6EA37DC6D87EA6B0 CRC64;  
 Query Match 47.8%; Score 11; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 W 1  
 Db 6 W 6

RESULT 7  
 TPFY\_PACDA STANDARD; PRT; 7 AA.  
 AC P83455;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Tryptophyllin-1 (PdT-1).  
 OS Pachymedusa dactinolor (Giant mexican leaf frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
 OC Phyllomedusinae; Pachymedusa.  
 OX NCBI\_TaxID=75988;  
 RN [1]  
 RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF  
 RP PRO-7.  
 RC TISSUE=Skin secretion;  
 RA Chen T.B., Orr D.F., Shaw C.;  
 RT "Pachymedusa dactinolor tryptophyllin-1 (PdT-1): structural  
 RT characterization, pharmacological activity and cloning of precursor  
 RT cDNA.";  
 RL Submitted (SEP-2002) to the SWISS-PROT data bank.  
 CC -1- FUNCTION: Myoactive. Has selective relaxing activity on vascular  
 CC smooth muscle.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Skin.  
 CC -1- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI.  
 DR GO: 0005576; C:extracellular; NAS.  
 DR GO: 0004596; P:negative regulation of smooth muscle contra. . .; NAS.  
 KW Amphibian defense peptide; Amidation; Hydroxylation.  
 FT MOD\_RES 3 3 HYDROXYLATION.  
 FT MOD\_RES 7 7 AMIDATION.  
 SQ SEQUENCE 7 AA; 794 MW; 7772D37DC776350 CRC64;  
 Query Match 47.8%; Score 11; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 W 1  
 Db 1

Db 5 W 5

RESULT 8  
 TY51\_LITRU STANDARD; PRT; 7 AA.  
 ID TY51\_LITRU  
 AC P82065;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Tryptophyllin 5.1.  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RP RP  
 RC TISSUE=Skin secretion;  
 RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,  
 RA Tyler M.J., Wallace J.C.;  
 RT "The structure of new peptides from the Australian red tree frog  
 RT 'Litoria rubella'. The skin peptide profile as a probe for the study  
 RT of evolutionary trends of amphibians.";  
 RL Aust. J. Chem. 49:955-963(1996).  
 CC -1- FUNCTION: May act as a neuromodulator or neurotransmitter.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
 CC -1- MASS SPECTROMETRY: MW=965; METHOD=PAB.  
 KW Amphibian defense peptide; Amidation; Neuropeptide;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 7 7 AMIDATION.  
 SQ SEQUENCE 7 AA; 983 MW; 7401E9D3676046B0 CRC64;  
 Query Match 47.8%; Score 11; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 W 1  
 Db 4 W 4

RESULT 9  
 WWAL\_ACHFU STANDARD; PRT; 7 AA.  
 ID WWAL\_ACHFU  
 AC P35919;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-OCT-1994 (Rel. 30, Last annotation update)  
 DE Wwamide-1.  
 OS Achatina fulica (Giant African snail).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
 OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.  
 OX NCBI\_TaxID=6530;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Ganglion;  
 RX MEDLINE=93265912; PubMed=8495720;  
 RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nonoto K.;  
 RT "Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from  
 RT ganglia of the African giant snail, *Achatina fulica*.";  
 RL FEBS Lett. 323:104-108(1993).  
 CC -1- FUNCTION: EXHIBITS MODULATORY EFFECTS ON THE PERIPHERAL NERVOUS  
 CC SYSTEM. INHIBITS ACTIVITY ON A CENTRAL NEURON.  
 DR PIR: S33245; S33245.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 7 7 AMIDATION.  
 SQ SEQUENCE 7 AA; 993 MW; 7362D5B69B041310 CRC64;  
 Query Match 47.8%; Score 11; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
Db 1 W 1

## RESULT 10

WAA2 ACHFU  
ID WAA2 ACHFU STANDARD; PRT; 7 AA.  
AC P35920;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-OCT-1994 (Rel. 30, Last annotation update)  
DE WAA2-2.  
OS Achatina fulica (Giant African snail).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Stylommatophora;  
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.  
OX NCBI\_TaxID=6530;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Ganglion;  
RX MEDLINE=93265912; PubMed=8495720;  
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;  
RT "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from  
RT ganglia of the African giant snail, Achatina fulica.";  
RL FEBS Lett. 323:104-108(1993).  
DR PIR: S33246; S33246.  
KW Neuropeptide; Amidation.  
FT MOD RES 7  
SQ SEQUENCE 7 AA; 964 MW; 7362D5B686D32310 CRC64;

Query Match 47.8%; Score 11; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
Db 1 W 1

## RESULT 11

WAA3 ACHFU  
ID WAA3 ACHFU STANDARD; PRT; 7 AA.  
AC P35921;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-OCT-1994 (Rel. 30, Last annotation update)  
DE WAA3-3.  
OS Achatina fulica (Giant African snail).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Stylommatophora;  
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.  
OX NCBI\_TaxID=6530;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Ganglion;  
RX MEDLINE=93265912; PubMed=8495720;  
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;  
RT "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from  
RT ganglia of the African giant snail, Achatina fulica.";  
RL FEBS Lett. 323:104-108(1993).  
DR PIR: S33244; S33244.  
KW Neuropeptide; Amidation.  
FT MOD RES 7  
SQ SEQUENCE 7 AA; 965 MW; 7362D5B69B132310 CRC64;

Query Match 47.8%; Score 11; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
Db 1 W 1

## RESULT 12

ACI THUAL STANDARD; PRT; 8 AA.  
AC P18691;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 01-NOV-1990 (Rel. 16, Last annotation update)  
DE Angiotensin-converting enzyme inhibitor.  
OS Thunnus albacares (Yellowfin tuna) (Neothunnus macropterus).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;  
OC Scombridae; Thunnus.  
OX NCBI\_TaxID=8236;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Muscle;  
RX MEDLINE=88326322; PubMed=3415688;  
RA Kohama Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura T.;  
RT "Isolation of angiotensin-converting enzyme inhibitor from tuna  
RT muscle.";  
RL Biochem. Biophys. Res. Commun. 155:332-337(1988).  
DR PIR: A31570; A31570.  
SQ SEQUENCE 8 AA; 953 MW; 6AA863733051F1B7 CRC64;

Query Match 47.8%; Score 11; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 W 1  
Db 6 W 6

## RESULT 13

AKHG GRYBI STANDARD; PRT; 8 AA.  
ID AKHG GRYBI  
AC P14086;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Adipokinetic hormone G (AKH-G) (80 II).  
OS Gryllus bimaculatus (Two-spotted cricket), and  
OS Romalea microptera (lubber grasshopper).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;  
OC Gryllus.  
OX NCBI\_TaxID=6999, 7007;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=G.bimaculatus; TISSUE=Corpora cardiaca;  
RX MEDLINE=88106553; PubMed=3426616;  
RA Gaede G., Rinehart K.L. Jr.;  
RT "Primary sequence analysis by fast atom bombardment mass spectrometry  
RT of a peptide with adipokinetic activity from the corpora cardiaca of  
RT the cricket Gryllus bimaculatus.";  
RL Biochem. Biophys. Res. Commun. 149:908-914(1987).  
RN [2]  
RP SEQUENCE.  
RC SPECIES=R.microptera; TISSUE=Corpora cardiaca;  
RX MEDLINE=89145002; PubMed=3226948;  
RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;  
RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from  
RT the lubber grasshopper, Romalea microptera.";  
RL Peptides 9:681-685(1988).  
CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA  
CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF  
CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT  
CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.  
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.  
DR PIR: A28004; A28004.

DR InterPro: IPR002047; AKH.  
DR PROSITE: PS00256; AKH; 1.  
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.  
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;

Query Match 47.8%; Score 11; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 W 1  
Db 8 W 8

## RESULT 14

AKH\_LIBAU STANDARD; PRT; 8 AA.  
AC P25418;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Adipokinetic hormone (AKH)  
OS Libellula auripennis (Skimmer dragonfly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Palaeoptera; Odonata; Anisoptera; Libellulidae; Libellula.  
OX NCBI\_TaxID=6966;

[1]  
RN RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Corpora cardiaca;  
RX MEDLINE=90359055; PubMed=2390213;  
RA Gaede G.;  
RT "The putative ancestral peptide of the adipokinetic/red-pigment-concentrating hormone family isolated and sequenced from a dragonfly."  
RL Biol. Chem. Hoppe-Seyler 371:475-483(1990).  
CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.  
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.

DR PIR; S10596; S10596.  
DR InterPro: IPR002047; AKH.  
DR PROSITE: PS00256; AKH; 1.  
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.  
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;

Query Match 47.8%; Score 11; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 W 1  
Db 8 W 8

## RESULT 15

AKH\_MELML STANDARD; PRT; 8 AA.  
AC P25423;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Adipokinetic hormone (AKH)  
OS Melolontha melolontha (Cockchafer), and  
OS Geotrupes stercorarius (Dor beetle), and  
OS Pachnoda marginata (flower beetle).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Scarabaeiformia;  
OC Scarabaeidae; Melolonthinae; Melolontha.

OX NCBI\_TaxID=7061, 7087, 7058;  
RN [1]  
RN SEQUENCE.  
RC SPECIES=M.melolontha, and G.stercorarius; TISSUE=Corpora cardiaca;  
RX MEDLINE=91248100; PubMed=2039445;  
RA Gaede G.;  
RT "A unique charged tyrosine-containing member of the adipokinetic hormone/red-pigment-concentrating hormone peptide family isolated and sequenced from two beetle species."  
RL Biochem. J. 275:671-677(1991).  
RN [2]

RN RP SEQUENCE.  
RC SPECIES=P.marginata; TISSUE=Corpora cardiaca;  
RX MEDLINE=92265187; PubMed=1586453;  
RA Gaede G., Lopata A., Kellner R., Rinehart K.L. Jr.;  
RT "Primary structures of neuropeptides isolated from the corpora cardiaca of various cetonid beetle species determined by pulsed-liquid phase sequencing and tandem fast atom bombardment mass spectrometry."  
RL Biol. Chem. Hoppe-Seyler 373:133-142(1992).  
CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.

CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.  
DR PIR; A58641; A58641.  
DR PIR; S15422; S15422.  
DR InterPro: IPR002047; AKH.  
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.  
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 1022 MW; 867AB775AB544736 CRC64;

Query Match 47.8%; Score 11; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 W 1  
Db 8 W 8

Search completed: January 12, 2004, 08:23:36  
Job time : 25 secs

```

> O <
O| |O IntelliGenetics
> O <

Quest - Quick User-directed Expression Search Tool
Release 5.4

-- Outline of search "seq1-iss" --

Selected search type is key against sequence data banks or files.
Selected scope is Sequence.
Selected sequence key from "new.key":
seq1 (AA) ID seq1 AA preliminary pattern
1
2 w
2 k or x
2 any character
2 any character
2 s or a
2 y or f
2 any character
2 g
2

Selected data banks and files:

Data bank : Issued_AA , all entries

-- Output Parameters --

Format Options:
Nucleic acid code matching Exact Indirect file
Find non-matching hits only No Sequence or key file
Report key used Yes List of hits
Note position of hit Yes Hit display
Display full annotations Yes Name and annotations
Sequence context 50

Run mode Batch
Time to start comparison now
Notify at end of run No

-- Run Parameters --

-----
1 match found in sequence:
US-08-608-241-2 ; Sequence 2, Application US/08608241
(from "/arch/iaa/5A.COMB.pep")
Sequence 2, Application US/08608241
Patent No. 5747328
GENERAL INFORMATION:
APPLICANT: Donohue, Timothy J
APPLICANT: Barber, Robert D
APPLICANT: Witthuhn, Vernon
TITLE OF INVENTION: MICROBIAL SYSTEM FOR FORMALDEHYDE
TITLE OF INVENTION: SENSING AND REMEDIATION
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/608,241
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/608,241
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296.93511
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
Found using 'seq1' (new.key)
...

-----
1 match found in sequence:
US-08-922-182-2 ; Sequence 2, Application US/08922182
(from "/arch/iaa/5B.COMB.pep")
Sequence 2, Application US/08922182
Patent No. 5834300
GENERAL INFORMATION:
APPLICANT: Donohue, Timothy J
APPLICANT: Barber, Robert D
APPLICANT: Witthuhn, Vernon
TITLE OF INVENTION: MICROBIAL SYSTEM FOR FORMALDEHYDE
TITLE OF INVENTION: SENSING AND REMEDIATION
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/922,182
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/608,241
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296.93511
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
Found using 'seq1' (new.key)
...

-----
1 match found in sequence:
US-08-922-182-2 ; Sequence 2, Application US/08922182
(from "/arch/iaa/5B.COMB.pep")
Sequence 2, Application US/08922182
Patent No. 5834300
GENERAL INFORMATION:
APPLICANT: Donohue, Timothy J
APPLICANT: Barber, Robert D
APPLICANT: Witthuhn, Vernon
TITLE OF INVENTION: MICROBIAL SYSTEM FOR FORMALDEHYDE
TITLE OF INVENTION: SENSING AND REMEDIATION
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/922,182
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/608,241
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296.93511
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
Found using 'seq1' (new.key)
...

-----
1 match found in sequence:
US-08-922-182-2 ; Sequence 2, Application US/08922182
(from "/arch/iaa/5B.COMB.pep")
Sequence 2, Application US/08922182
Patent No. 5834300
GENERAL INFORMATION:
APPLICANT: Donohue, Timothy J
APPLICANT: Barber, Robert D
APPLICANT: Witthuhn, Vernon
TITLE OF INVENTION: MICROBIAL SYSTEM FOR FORMALDEHYDE
TITLE OF INVENTION: SENSING AND REMEDIATION
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/922,182
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/608,241
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296.93511
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
Found using 'seq1' (new.key)
...

```

266 YTPDCTGNVKNRQALEACHRGWGQSVIGVAPAGAEIQTRPQLVTGRVWKGSAFGGAR 316 323  
-----|

326 GRTDVPKIVDWMYMEGKIQIDPMITHILSLSEINKGFDLMHAGESIRSV

-----  
1 match found in sequence:  
US-08-919-953-2 ; Sequence 2, Application US/08919953  
(from "/arch/iaa/5B COMB.pep")  
Sequence 2, Application US/08919953  
Patent No. 5817481

GENERAL INFORMATION:  
APPLICANT: Donohue, Timothy J  
APPLICANT: Barber, Robert D  
APPLICANT: Witthuhn, Vernon  
TITLE OF INVENTION: MICROBIAL SYSTEM FOR FORMALDEHYDE  
TITLE OF INVENTION: SENSING AND REMEDIATION  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Quarles & Brady  
STREET: 1 South Pinckney Street  
CITY: Madison  
STATE: WI  
COUNTRY: US

ZIP: 53703  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/919,953  
FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/608,241

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Seay, Nicholas J

REGISTRATION NUMBER: 27,386

REFERENCE/DOCKET NUMBER: 960296.93511

TELECOMMUNICATION INFORMATION:

TELEPHONE: 608-251-5000

TELEFAX: 608-251-9166

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 376 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

Found using 'seq1' (new.key)

266 YTPDCTGNVKNRQALEACHRGWGQSVIGVAPAGAEIQTRPQLVTGRVWKGSAFGGAR 316 323  
-----|

326 GRTDVPKIVDWMYMEGKIQIDPMITHILSLSEINKGFDLMHAGESIRSV

-----  
1 match found in sequence:  
US-08-637-759B-89 ; Sequence 89, Application US/08637759B  
(from "/arch/iaa/5B COMB.pep")  
Sequence 89, Application US/08637759B  
Patent No. 5876931  
GENERAL INFORMATION:

APPLICANT: David William Holden  
TITLE OF INVENTION: Identification of Genes  
NUMBER OF SEQUENCES: 501  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patrea L. Pabst  
STREET: 2800 One Atlantic Center  
STREET: 1201 West Peachtree Street  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30309-3450  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/637,759B

FILING DATE: 03-MAY-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB95/02875

FILING DATE: 11-DEC-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Pabst, Patrea L.

REGISTRATION NUMBER: 31,284

REFERENCE/DOCKET NUMBER: RPMS 101

TELECOMMUNICATION INFORMATION:

TELEPHONE: (404) 873-8794

TELEFAX: (404) 873-8795

INFORMATION FOR SEQ ID NO: 89:

SEQUENCE CHARACTERISTICS:

LENGTH: 759 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

Found using 'seq1' (new.key)

1 NYTHGRILLCQILKQTFLEDELLFKALANWKPAPFGIPQRLFLRLDGLAMSCSPPLSSS 30 37  
-----|

61 AELWLRLHHRQIKFXGVAMRSLWEGEV

-----  
1 match found in sequence:  
US-08-871-355A-89 ; Sequence 89, Application US/08871355A  
(from "/arch/iaa/6A COMB.pep")  
Sequence 89, Application US/08871355A  
Patent No. 6015669

GENERAL INFORMATION:

APPLICANT: David William Holden

TITLE OF INVENTION: Identification of Genes

NUMBER OF SEQUENCES: 501

CORRESPONDENCE ADDRESS:

ADDRESSEE: Patrea L. Pabst

STREET: 2800 One Atlantic Center

STREET: 1201 West Peachtree Street

CITY: Atlanta

STATE: Georgia

COUNTRY: USA

ZIP: 30309-3450

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/871,355A  
FILING DATE: 09-JUN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB95/02875  
FILING DATE: 11-DEC-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: RPLMS 101 CON  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404) 873-8794  
TELEFAX: (404) 873-8795  
INFORMATION FOR SEQ ID NO: 89:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 759 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
Found using 'seq1' (new.key)

1 NYHNGRILLCQILKQTLDEILLFKALANWKPAAFGIPIQLFLLRDGLAMSCSPPLSSS  
30 37

61 AELMLRLHHRQIKFXGVAMRWLGEV

...

1 match found in sequence:  
US-09-222-817-2 : Sequence 2, Application US/09222817  
(from "/arch/iaa/6A.COMB.pep")  
Sequence 2, Application US/09222817  
Patent No. 6037154  
GENERAL INFORMATION:  
APPLICANT: Mikiko SUGA, Masakazu SUGIMOTO, Tsuyoshi OSUMI, Tsuyoshi NAKAMATSU,  
TITLE OF INVENTION: METHOD OF PRODUCING L-SERINE BY FERMENTATION  
FILE REFERENCE: OP813  
CURRENT APPLICATION NUMBER: US/09/222,817  
CURRENT FILING DATE: 1998-12-30  
EARLIER APPLICATION NUMBER: JP 10-3751  
EARLIER FILING DATE: 1998-01-12  
EARLIER APPLICATION NUMBER: JP 10-353521  
EARLIER FILING DATE: 1998-12-11  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 345  
TYPE: PRT  
ORGANISM: Corynebacterium glutamicum  
Found using 'seq1' (new.key)

82 VDI PAATEAGVMVANAPTSNIHSAEHAISLLSTARQIPAAATLREGEWKRSFNGVE  
132 139

142 IFGKTVGIVGFHGIGQLFAQRLAAAFETTIVAYDPYANPARAAQLNVEL

...

1 match found in sequence:  
US-09-222-817-12 : Sequence 12, Application US/09222817  
(from "/arch/iaa/6A.COMB.pep")  
Sequence 12, Application US/09222817  
Patent No. 6037154  
GENERAL INFORMATION:  
APPLICANT: Donohue, Timothy  
APPLICANT: Barber, Robert  
APPLICANT: Witthuhn, Vernon  
TITLE OF INVENTION: Microbial System for Formaldehyde Sensing and  
Remediation

APPLICANT: Mikiko SUGA, Masakazu SUGIMOTO, Tsuyoshi OSUMI, Tsuyoshi NAKAMATSU,  
TITLE OF INVENTION: METHOD OF PRODUCING L-SERINE BY FERMENTATION  
FILE REFERENCE: OP813  
CURRENT APPLICATION NUMBER: US/09/222,817  
CURRENT FILING DATE: 1998-12-30  
EARLIER APPLICATION NUMBER: JP 10-3751  
EARLIER FILING DATE: 1998-01-12  
EARLIER APPLICATION NUMBER: JP 10-353521  
EARLIER FILING DATE: 1998-12-11  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 12  
LENGTH: 530  
TYPE: PRT  
ORGANISM: Brevibacterium flavum  
Found using 'seq1' (new.key)

...

82 VDI PAATEAGVMVANAPTSNIHSAEHAISLLSTARQIPAAATLREGEWKRSFNGVE  
132 139

142 IFGKTVGIVGFHGIGQLFAQRLAAAFETTIVAYDPYANPARAAQLNVEL

...

1 match found in sequence:  
US-09-222-817-14 : Sequence 14, Application US/09222817  
(from "/arch/iaa/6A.COMB.pep")  
Sequence 14, Application US/09222817  
Patent No. 6037154  
GENERAL INFORMATION:  
APPLICANT: Mikiko SUGA, Masakazu SUGIMOTO, Tsuyoshi OSUMI, Tsuyoshi NAKAMATSU,  
TITLE OF INVENTION: METHOD OF PRODUCING L-SERINE BY FERMENTATION  
FILE REFERENCE: OP813  
CURRENT APPLICATION NUMBER: US/09/222,817  
CURRENT FILING DATE: 1998-12-30  
EARLIER APPLICATION NUMBER: JP 10-3751  
EARLIER FILING DATE: 1998-01-12  
EARLIER APPLICATION NUMBER: JP 10-353521  
EARLIER FILING DATE: 1998-12-11  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 14  
LENGTH: 530  
TYPE: PRT  
ORGANISM: Brevibacterium flavum  
Found using 'seq1' (new.key)

...

82 VDI PAATEAGVMVANAPTSNIHSAEHAISLLSTARQIPAAATLREGEWKRSFNGVE  
132 139

142 IFGKTVGIVGFHGIGQLFAQRLAAAFETTIVAYDPYANPARAAQLNVEL

...

1 match found in sequence:  
US-09-192-983-2 : Sequence 2, Application US/09192983A  
(from "/arch/iaa/6A.COMB.pep")  
Sequence 2, Application US/09192983A  
Patent No. 6242244  
GENERAL INFORMATION:  
APPLICANT: Donohue, Timothy  
APPLICANT: Barber, Robert  
APPLICANT: Witthuhn, Vernon  
TITLE OF INVENTION: Microbial System for Formaldehyde Sensing and  
Remediation

FILE REFERENCE: 960296.95505  
CURRENT APPLICATION NUMBER: US/09/192,983A  
CURRENT FILING DATE: 1998-11-16  
EARLIER APPLICATION NUMBER: 08/919,953  
EARLIER FILING DATE: 1997-08-29  
EARLIER APPLICATION NUMBER: 08/608,241  
EARLIER FILING DATE: 1996-02-28  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 376  
TYPE: PRT  
ORGANISM: Rhodobacter sphaeroides  
Found using 'seq1' (new.key)

...  
266 YTFDCTGNVKMRQALEACHRGWGQSIIVGAPAGABIQTRPQLVTGRVWKGSAFGGAR 316  
323

326 GRTDVPKIVDWMYMEGKIQIDPMITHLSLEINKGPDLMHAGESIRSV

...  
-----  
1 match found in sequence:  
US-09-222-786-2 ; Sequence 2, Application US/09222786A  
(from "/arch/iaa/6A COMB.pep")  
Sequence 2, Application US/09222786A  
Patent No. 6258573  
GENERAL INFORMATION:  
APPLICANT: Mikiko SUGA, Masakazu SUGIMOTO, Tsuyoshi OSUMI, Tsuyoshi NAKAMATSU,  
TITLE OF INVENTION: METHOD OF PRODUCING L-SERINE BY FERMENTATION  
FILE REFERENCE: OP812  
CURRENT APPLICATION NUMBER: US/09/222,786A  
CURRENT FILING DATE: 1998-12-30  
EARLIER APPLICATION NUMBER: JP 10-3751  
EARLIER FILING DATE: 1998-01-12  
EARLIER APPLICATION NUMBER: JP 10-353513  
EARLIER FILING DATE: 1998-12-11  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 345  
TYPE: PRT  
ORGANISM: Corynebacterium glutamicum  
Found using 'seq1' (new.key)

...  
82 VDIPATEAGVMVANAPTNIHSACEHAISLLSTARQIPAADATLREGWKRSFNGVE 132  
139

142 IFGKTVGIVGFHIGQLFAQLAFAFETTIVAYDPYANPARAAQLNVEL

...  
-----  
1 match found in sequence:  
US-09-222-786-12 ; Sequence 12, Application US/09222786A  
(from "/arch/iaa/6A COMB.pep")  
Sequence 12, Application US/09222786A  
Patent No. 6258573  
GENERAL INFORMATION:  
APPLICANT: Mikiko SUGA, Masakazu SUGIMOTO, Tsuyoshi OSUMI, Tsuyoshi NAKAMATSU,  
TITLE OF INVENTION: METHOD OF PRODUCING L-SERINE BY FERMENTATION  
FILE REFERENCE: OP812  
CURRENT APPLICATION NUMBER: US/09/222,786A  
CURRENT FILING DATE: 1998-12-30  
EARLIER APPLICATION NUMBER: JP 10-3751  
EARLIER FILING DATE: 1998-01-12

EARLIER APPLICATION NUMBER: JP 10-353513  
EARLIER FILING DATE: 1998-12-11  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 12  
LENGTH: 530  
TYPE: PRT  
ORGANISM: Brevibacterium flavum  
Found using 'seq1' (new.key)

...  
82 VDIPATEAGVMVANAPTNIHSACEHAISLLSTARQIPAADATLREGWKRSFNGVE 132  
139

142 IFGKTVGIVGFHIGQLFAQLAFAFETTIVAYDPYANPARAAQLNVEL

...  
-----  
1 match found in sequence:  
US-09-222-786-14 ; Sequence 14, Application US/09222786A  
(from "/arch/iaa/6A COMB.pep")  
Sequence 14, Application US/09222786A  
Patent No. 6258573  
GENERAL INFORMATION:  
APPLICANT: Mikiko SUGA, Masakazu SUGIMOTO, Tsuyoshi OSUMI, Tsuyoshi NAKAMATSU,  
TITLE OF INVENTION: METHOD OF PRODUCING L-SERINE BY FERMENTATION  
FILE REFERENCE: OP812  
CURRENT APPLICATION NUMBER: US/09/222,786A  
CURRENT FILING DATE: 1998-12-30  
EARLIER APPLICATION NUMBER: JP 10-3751  
EARLIER FILING DATE: 1998-01-12  
EARLIER APPLICATION NUMBER: JP 10-353513  
EARLIER FILING DATE: 1998-12-11  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 14  
LENGTH: 530  
TYPE: PRT  
ORGANISM: Brevibacterium flavum  
Found using 'seq1' (new.key)

...  
82 VDIPATEAGVMVANAPTNIHSACEHAISLLSTARQIPAADATLREGWKRSFNGVE 132  
139

142 IFGKTVGIVGFHIGQLFAQLAFAFETTIVAYDPYANPARAAQLNVEL

...  
-----  
1 match found in sequence:  
US-09-516-143A-2 ; Sequence 2, Application US/09516143A  
(from "/arch/iaa/6B COMB.pep")  
Sequence 2, Application US/09516143A  
Patent No. 6333182  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc.  
TITLE OF INVENTION: Human Glycosylation Enzymes  
FILE REFERENCE: PF505PCT  
CURRENT APPLICATION NUMBER: US/09/516,143A  
CURRENT FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: 60/122,409  
PRIOR FILING DATE: 1999-03-02  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 434  
TYPE: PRT

```
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: 133
OTHER INFORMATION: Xaa equals Tyr or His
NAME/KEY: SITE
LOCATION: 136
OTHER INFORMATION: Xaa equals Gly or Val
NAME/KEY: SITE
LOCATION: 147
OTHER INFORMATION: Xaa equals Ser or Pro
NAME/KEY: SITE
LOCATION: 169
OTHER INFORMATION: Xaa equals Gly or Val
Found using 'seq1' (new.key)
...
315 KKGIEVRLISRACSKOTLSSKLDCRMEVSVSKLAVVDEWRKEMGLCWKEVAYLNE
365 372
375 VSDERCLXVGLSGAPADACSAQAQAVGYCKNGRGRAIRFABHIC
...
1 match found in sequence:
US-09-201-945-89 ; Sequence 89, Application US/09201945
(from "/srch/1aa/6B-COMB.pep")
Sequence 89, Application US/09201945
Patent No. 6342215
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/201,945
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/637,759
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS 101
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 759 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
Found using 'seq1' (new.key)

1 NYHNGRILLCOILKQTLDEBLLFKALANWKPAAFQGIQPORLFLLRDGLAMSCSPPLSSS
30 37
61 AELWLRLHHRQIKFXGVAMRSWLGEV
...
1 match found in sequence:
US-09-347-878-54 ; Sequence 54, Application US/09347878C
(from "/srch/1aa/6B-COMB.pep")
Sequence 54, Application US/09347878C
Patent No. 6376210
GENERAL INFORMATION:
APPLICANT: Yuan, Chong
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
FILE REFERENCE: 25885-1651
CURRENT APPLICATION NUMBER: US/09/347,878C
CURRENT FILING DATE: 1999-07-06
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 54
LENGTH: 374
TYPE: PRT
ORGANISM: Homo sapiens
Found using 'seq1' (new.key)
...
264 YSFECIGNVKVMRAALEACHKRGVSVVVGVAASGEIATPFPQVLTGRTWKGTAFGGMK
314 321
324 SVESVPLVSEYMSKKIKVDFVTHNLSPDEINKAFELMHSGKSIRTV
...
1 match found in sequence:
US-09-324-541-11 ; Sequence 11, Application US/09324541
(from "/srch/1aa/6B-COMB.pep")
Sequence 11, Application US/09324541
Patent No. 6391855
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
JUNCTIONAL ADHESION MOLECULE-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.412
CURRENT APPLICATION NUMBER: US/09/324,541
CURRENT FILING DATE: 1999-06-02
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 11
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Fab fragment directed against claudin cell
adhesion recognition sequence
Found using 'seq1' (new.key)
...
1 WKIYSYAG
8
1 match found in sequence:
US-09-130-491-4 ; Sequence 4, Application US/09130491
(from "/srch/1aa/6B-COMB.pep")
Sequence 4, Application US/09130491
```

Patent No. 6416974  
GENERAL INFORMATION:  
APPLICANT: Holtzman, Douglas A.  
APPLICANT: Goodearl, Andrew D.J.  
TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83  
FILE REFERENCE: 09404/041001  
CURRENT APPLICATION NUMBER: US/09/130,491  
CURRENT FILING DATE: 1998-08-07  
EARLIER APPLICATION NUMBER: US 60/058,108  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: US 60/054,961  
EARLIER FILING DATE: 1997-08-06  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 4  
LENGTH: 211  
TYPE: PRT  
ORGANISM: Homo sapiens  
Found using 'seq1' (new.key)

1 MANAGLQLGLFILAFILGWIGAVSTALPQWRIYSYAGDNIVTAQMYEGLWMSVCVSQSTG  
30 37  
-----|-----|  
61 QIQCKVFDLSLNLSTLOATRALMVVG  
....  
-----  
1 match found in sequence:  
US-09-130-491-15 ; Sequence 15, Application US/09130491  
(from "/arch/iaa/6B\_COMB.pep")  
Sequence 15, Application US/09130491  
Patent No. 6416974  
GENERAL INFORMATION:  
APPLICANT: Holtzman, Douglas A.  
APPLICANT: Goodearl, Andrew D.J.  
TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83  
FILE REFERENCE: 09404/041001  
CURRENT APPLICATION NUMBER: US/09/130,491  
CURRENT FILING DATE: 1998-08-07  
EARLIER APPLICATION NUMBER: US 60/058,108  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: US 60/054,961  
EARLIER FILING DATE: 1997-08-06  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 15  
LENGTH: 247  
TYPE: PRT  
ORGANISM: Homo sapiens  
Found using 'seq1' (new.key)

1 MMSLEITGTSLAVLWGLCTIVCCALPMWRVSAFISGSIITAITWGLWMNCVQSTGM  
29 36  
-----|-----|  
61 QCKWYDLSLLALPDQLQARALIVSI  
....  
-----  
1 match found in sequence:  
US-09-724-623-110 ; Sequence 110, Application US/09724623  
(from "/arch/iaa/6B\_COMB.pep")  
Sequence 110, Application US/09724623  
Patent No. 6476209  
GENERAL INFORMATION:  
APPLICANT: Glenn, Matthew  
APPLICANT: Lubbers, Mark W  
APPLICANT: Dekker, James  
TITLE OF INVENTION: Polynucleotides, materials incorporating  
TITLE OF INVENTION: them, and methods for using them.

FILE REFERENCE: 1048U1  
CURRENT APPLICATION NUMBER: US/09/724,623  
CURRENT FILING DATE: 2000-11-28  
NUMBER OF SEQ ID NOS: 124  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 110  
LENGTH: 306  
TYPE: PRT  
ORGANISM: Lactobacillus rhamnosus  
Found using 'seq1' (new.key)

129 FSNLPQGMCPCTCOGLGYVDDIDVSKLIDPNKSLNQEAITFVSFGPDTWRWRVAYSGLF  
-----|-----|  
179 186  
189 DNDKPLRDYTPPEMKLLLYAPQOTLKHPAKWPRALYEGVVPRKRS  
....  
-----  
1 match found in sequence:  
US-08-976-063E-8 ; Sequence 8, Application US/08976063E  
(from "/arch/iaa/6B\_COMB.pep")  
Sequence 8, Application US/08976063E  
Patent No. 6524831  
GENERAL INFORMATION:  
APPLICANT: Steinbuechel, Alexander  
APPLICANT: Priefert, Horst  
TITLE OF INVENTION: SYNTHETIC ENZYMES FOR THE PRODUCTION OF CONIFERYL  
TITLE OF INVENTION: ALCOHOL, CONIFERYLALDEHYDE, FERULIC ACID, VANILLIN AND  
TITLE OF INVENTION: VANILLIC ACID AND THEIR USE  
FILE REFERENCE: Bayer-9998-CAC  
CURRENT APPLICATION NUMBER: US/08/976,063E  
CURRENT FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 196 49 655.1 GERMANY  
PRIOR FILING DATE: 1996-11-29  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 8  
LENGTH: 372  
TYPE: PRT  
ORGANISM: not required under old rule  
Found using 'seq1' (new.key)

260 YSFCIGNVRLMRAALECCHKWGESVIIGVAPAGAEINTRPFHLVTRVWRVSGSFGVK  
-----|-----|  
310 317  
320 GRTELPYVEKAQCGEIPLDTFITHTMGLDDINTAFDLMDEGKSIRSV  
....  
-----  
1 match found in sequence:  
US-09-205-258-344 ; Sequence 344, Application US/09205258  
(from "/arch/iaa/6B\_COMB.pep")  
Sequence 344, Application US/09205258  
Patent No. 6525174  
GENERAL INFORMATION:  
APPLICANT: Young et al.  
TITLE OF INVENTION: 207 Human Secreted Proteins  
FILE REFERENCE: P2007P1  
CURRENT APPLICATION NUMBER: US/09/205,258  
CURRENT FILING DATE: 1998-12-04  
EARLIER APPLICATION NUMBER: PCT/US98/11422  
EARLIER FILING DATE: 1998-06-04  
EARLIER APPLICATION NUMBER: 60/048,885  
EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/049,375  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,881  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,880  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,896  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,020  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,876  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,895  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,884  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,894  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,900  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,901  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,892  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,915  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,019  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,970  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,972  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,916  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,373  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,875  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,374  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,917  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,949  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,883  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,897  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,898  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,962  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,963  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,877  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,878  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/070,923  
EARLIER FILING DATE: 1997-12-18  
EARLIER APPLICATION NUMBER: 60/092,921

EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/094,657  
EARLIER FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 1227  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 344  
LENGTH: 202  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (202)  
OTHER INFORMATION: Xaa equals stop translation  
Found using 'seq1' (new key)

1 MGIALAVLGWLAVMLCCALPMWRVTAFIGSNIVTSQTIWEGLLMNCVVQSTGQMCKKYD  
22 29  
61 SLLALPDQLQARALVIIS  
...

-----  
1 match found in sequence:  
US-09-205-258-463 ; Sequence 463, Application US/09205258  
(from "/srch/iaa/6B COMB.pep")  
Sequence 463, Application US/09205258  
Patent No. 6525174  
GENERAL INFORMATION:  
APPLICANT: Young et al.  
TITLE OF INVENTION: 207 Human Secreted Proteins  
FILE REFERENCE: P2007P1  
CURRENT APPLICATION NUMBER: US/09/205,258  
CURRENT FILING DATE: 1998-12-04  
EARLIER APPLICATION NUMBER: PCT/US98/11422  
EARLIER FILING DATE: 1998-06-04  
EARLIER APPLICATION NUMBER: 60/048,885  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,375  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,881  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,880  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,896  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,020  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,876  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,895  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,884  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,894  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,971  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,882  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,899  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,893  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,900  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,901  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,892  
EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,915  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,019  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,970  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,972  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,916  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,373  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,875  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,374  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,917  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,949  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,883  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,897  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,898  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,962  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,963  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,877  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,878  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/070,923  
EARLIER FILING DATE: 1997-12-18  
EARLIER APPLICATION NUMBER: 60/092,921  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/094,657  
EARLIER FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 1227  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 463  
LENGTH: 206  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (80)  
OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (93)  
OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (206)  
OTHER INFORMATION: xaa equals stop translation  
Found using 'seq1' (new.key)

142 SLMNTWPTVISAFANDPVDVTREATSSVLLPLDGGDRVSLRLRRGNLLGWKYSFSGFL  
192 199

202 IFPLX

1 match found in sequence:  
US-09-252-991A-18795 ; Sequence 18795, Application US/09252991A

(from "/arch/iaa/6B\_COMB.pep")  
Sequence 18795, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 18795  
LENGTH: 334  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
Found using 'seq1' (new.key)

50 PVPAPCLOAPASLLSTAPTATWADFLINALLAGLALVALVAGPLGSGFVWRMAYFGDT  
100 107

110 LSHAALLGVALGFLLDVSPTLATVTGCVLLAVLLVTLQORQPLAADTL

1 match found in sequence:  
US-09-252-991A-20880 ; Sequence 20880, Application US/09252991A  
(from "/arch/iaa/6B\_COMB.pep")  
Sequence 20880, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 20880  
LENGTH: 375  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
Found using 'seq1' (new.key)

305 SRSGLLQGRQALDRQVRVATDFRADMRGOLAQGVGGTHQRSWFIRSIITWRVMSYCGLT  
355 362

365 STTAPRSMTMS

1 match found in sequence:  
US-09-252-991A-21227 ; Sequence 21227, Application US/09252991A  
(from "/arch/iaa/6B\_COMB.pep")  
Sequence 21227, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 20880  
LENGTH: 375  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
Found using 'seq1' (new.key)

305 SRSGLLQGRQALDRQVRVATDFRADMRGOLAQGVGGTHQRSWFIRSIITWRVMSYCGLT  
355 362

365 STTAPRSMTMS

1 match found in sequence:  
US-09-252-991A-21227 ; Sequence 21227, Application US/09252991A  
(from "/arch/iaa/6B\_COMB.pep")  
Sequence 21227, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 20880  
LENGTH: 375  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
Found using 'seq1' (new.key)

FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
PRIOR FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 21227  
LENGTH: 399  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
Found using 'seq1' (new.key)

...

289 YSFECVGNVQLMRAALECCKGWSVIIGVAGAGOEISTRPQLVTGRVWGSAGGYR 339 346  
-----|-----|

349 GRSELPYVEKAQGEIPLDTFTTHMGLEDINEAFELMHGKSIRTV 339 346  
-----|-----|

1 match found in sequence:  
US-09-252-991A-22187 ; Sequence 22187, Application US/09252991A  
(from "/arch/iaa/6B\_COMB.pep")  
Sequence 22187, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 22187  
LENGTH: 728  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
FEATURE:  
NAME/KEY: UNSURE  
LOCATION: (699)  
OTHER INFORMATION: Identity of amino acid at the above locations are unknown.  
Found using 'seq1' (new.key)

1 SRRAPALSRIIRTVRTARGGPQWIRPAPFGAACRGLPGRHGRGRLVSPGARR 27 34  
-----|-----|

61 SRQRPAGTSGAGEYGSGLLPAR 34  
-----|-----|

1 match found in sequence:  
US-09-252-991A-25507 ; Sequence 25507, Application US/09252991A  
(from "/arch/iaa/6B\_COMB.pep")  
Sequence 25507, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 25507  
LENGTH: 447  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
Found using 'seq1' (new.key)

...

23 OPDGPSTRKRSAGSTSKLRWVARTTRRVYSLRTPSTASRASAGSVEGWREAAFIGVS 73 80  
-----|-----|

83 TPLQRRVLEBIVLPGRLVADRTDPVEKLQRICGLVLRDAELHLIRIG 73 80  
-----|-----|

1 match found in sequence:  
US-09-252-991A-25705 ; Sequence 25705, Application US/09252991A  
(from "/arch/iaa/6B\_COMB.pep")  
Sequence 25705, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 25705  
LENGTH: 547  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
Found using 'seq1' (new.key)

...

414 SLLPFVHGAPPADWRRYVIAIEYVAFQAPARERLGRPIDACRMVVRSEWKYIAYDGFR 464 471  
-----|-----|

474 AQLPDLASDPGELRDLCNDPAHAHVREAHAGMLFDWLRLGLKRTTISN 464 471  
-----|-----|

1 match found in sequence:  
US-09-252-991A-29231 ; Sequence 29231, Application US/09252991A  
(from "/arch/iaa/6B\_COMB.pep")  
Sequence 29231, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 29231  
LENGTH: 426  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
Found using 'seq1' (new.key)

66 PAFRGQPVRRSAGTAGDSDGSPSRTRLPEAIHLPGRRKARLKPPRWRSAAPDGS  
116 123

126 GRLEGAAPLVAFLARSDAEVAVGAGEMRPGRETAGQADLDRLAG

1 match found in sequence:  
US-09-328-352-5472 ; Sequence 5472, Application US/09328352  
(from "/arch/iaa/6B COMB.pep")  
Sequence 5472, Application US/09328352  
Patent No. 6562958  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
(from "/arch/iaa/6B COMB.pep")  
FILE REFERENCE: GTC99-03PA  
CURRENT APPLICATION NUMBER: US/09/328,352  
CURRENT FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 8252  
SEQ ID NO 5472  
LENGTH: 192  
TYPE: PRT  
ORGANISM: Acinetobacter baumannii  
Found using 'seq1' (new.key)

35 NIKADLLNAEDLTSSGILQYDGLWGSPTYLGVSCKLQKLDATGFLWKKQSPKGL  
85 92

95 AGFTVSSLPAGDKQSTLIISIFTCMQHGMLWGNPILPEOHQGVAYT

1 match found in sequence:  
US-09-663-600A-92 ; Sequence 92, Application US/09663600A  
(from "/arch/iaa/6B COMB.pep")  
Sequence 92, Application US/09663600A  
Patent No. 6573068  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
APPLICANT: Duclert, Aymeric  
APPLICANT: Bougueleret, Lydie  
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS  
FILE REFERENCE: 31.US3.CIP  
CURRENT APPLICATION NUMBER: US/09/663,600A  
CURRENT FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: 09/191,997  
PRIOR FILING DATE: 1998-11-13  
PRIOR APPLICATION NUMBER: 60/066,677  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/069,957  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/074,121  
PRIOR FILING DATE: 1998-02-09  
PRIOR APPLICATION NUMBER: 60/081,563  
PRIOR FILING DATE: 1998-04-13  
PRIOR APPLICATION NUMBER: 60/096,116  
PRIOR FILING DATE: 1998-08-10  
PRIOR APPLICATION NUMBER: 60/099,273  
PRIOR FILING DATE: 1998-11-13

PRIOR FILING DATE: 1998-09-04  
NUMBER OF SEQ ID NOS: 229  
SOFTWARE: Patent.pm  
SEQ ID NO 92  
LENGTH: 230  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: -24...-1  
NAME/KEY: UNSURE  
LOCATION: 54,79  
OTHER INFORMATION: Xaa = any one of the twenty amino acids  
Found using 'seq1' (new.key)

1 MASLGLQLVGYILGLLGLTLVAMLLPSWKTSYVVGASIVTAVGFSKGLMMECATHTSG  
30 37

61 ITQCDIYSTLLGLLPADIQAQAMMVT

1 match found in sequence:  
US-09-663-600A-186 ; Sequence 186, Application US/09663600A  
(from "/arch/iaa/6B COMB.pep")  
Sequence 186, Application US/09663600A  
Patent No. 6573068  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
APPLICANT: Duclert, Aymeric  
APPLICANT: Bougueleret, Lydie  
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS  
FILE REFERENCE: 31.US3.CIP  
CURRENT APPLICATION NUMBER: US/09/663,600A  
CURRENT FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: 09/191,997  
PRIOR FILING DATE: 1998-11-13  
PRIOR APPLICATION NUMBER: 60/066,677  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/069,957  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/074,121  
PRIOR FILING DATE: 1998-02-09  
PRIOR APPLICATION NUMBER: 60/081,563  
PRIOR FILING DATE: 1998-04-13  
PRIOR APPLICATION NUMBER: 60/096,116  
PRIOR FILING DATE: 1998-08-10  
PRIOR APPLICATION NUMBER: 60/099,273  
PRIOR FILING DATE: 1998-09-04  
NUMBER OF SEQ ID NOS: 229  
SOFTWARE: Patent.pm  
SEQ ID NO 186  
LENGTH: 230  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: -24...-1  
Found using 'seq1' (new.key)

1 MASLGLQLVGYILGLLGLTLVAMLLPSWKTSYVVGASIVTAVGFSKGLMMECATHTSG  
30 37

61 ITQCDIYSTLLGLLPADIQAQAMMVT

1 match found in sequence:  
US-09-732-210-332 ; Sequence 332, Application US/09732210

```
(from "/srch/iaa/6B_COMB.pep")
Sequence 332, Application US/09732210
Patent No. 6573361
GENERAL INFORMATION:
APPLICANT: Bunkers, Greg J.
APPLICANT: Liang, Jihong
APPLICANT: Mittanck, Cindy A.
APPLICANT: Seale, Jeffrey W.
APPLICANT: Wu, Yonnie S.
TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
FILE REFERENCE: 38-21(15036)B
CURRENT APPLICATION NUMBER: US/09/732,210
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/169,513
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: US 60/169,340
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 1753
SEQ ID NO 332
LENGTH: 70
TYPE: PRT
ORGANISM: Methanococcus jannaschii
Found using 'seq1' (new.key)
1 1 MPEWRTCSFCGYE1BPGKGMVVEKDTLVYFCSSKCEKSYRMGRNPKLKWTKVYQDMK
4 11
61 A
...
-----
1 match found in sequence:
US-09-107-532A-7233 ; Sequence 7233, Application US/09107532A
(from "/srch/iaa/6B_COMB.pep")
Sequence 7233, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESS: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Walham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 7233:
SEQUENCE CHARACTERISTICS:
LENGTH: 354 amino acids
TYPE: amino acid
MOLECULE TYPE: linear
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...68
SEQUENCE DESCRIPTION: SEQ ID NO: 7233:
Found using 'seq1' (new.key)
```

```
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...354
SEQUENCE DESCRIPTION: SEQ ID NO: 7233:
Found using 'seq1' (new.key)
1 1 IIKLGRRMKLLKLLFTVSALLLTGTLACGSGSKDQAEASNSDTLQMYQIGDKPDNF
12 19
61 DQLMVANK
...
-----
1 match found in sequence:
US-09-107-532A-7307 ; Sequence 7307, Application US/09107532A
(from "/srch/iaa/6B_COMB.pep")
Sequence 7307, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESS: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Walham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 7307:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
TYPE: amino acid
MOLECULE TYPE: linear
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...68
SEQUENCE DESCRIPTION: SEQ ID NO: 7307:
Found using 'seq1' (new.key)
```

Number of sequence hits saved: 0

6 HPIEENKRYSAKQRQSVKRLTRCSNKADRRKLVILKKSTHNNRKLWKRYSYIGRI 56  
-----|-----|  
66 RIS 63

-----  
1 match found in sequence:  
US-09-215-418-2 ; Sequence 2, Application US/09215418  
(from "farch/iaa/6B COMB.pep")  
Sequence 2, Application US/09215418  
Patent No. 6586217  
GENERAL INFORMATION:  
APPLICANT: Guimaraes, M. Jorge  
APPLICANT: Bazan, J. Fernando  
APPLICANT: Zlotnik, Albert  
TITLE OF INVENTION: MAMMALIAN SELENOPHOSPHATE SYNTHETASE  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/215,418  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/406,359  
FILING DATE: 17-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0493  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-852-9196  
TELEFAX: 415-496-1200  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 452 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
Found using 'seq1' (new.key)

2 AAAAAAGSGETWAALVAEAGSLGACGWSAGRSFNSYRPFEPQTLGFSPSMRLTSPSGMK 52  
-----|-----|  
59

62 GCGCKVPQETLLKLEGLTRPALQPLTSLGLVGQGETVQEGGLSTRP

-- Search Statistics --

Times: CPU Total Elapsed  
00:01:33.10 00:01:41.00

Number of sequences searched: 328807  
Number of sequence hits: 36  
Number of separate matches: 36

! FINDPATTERNS on pir:\* allowing 0 mismatches

```
! 1 W(K,R)XX(S,A)(Y,F)XG January 12, 2004 10:19 ..
DEHUC2 ck: 9148 len: 374 | alcohol dehydrogenase (EC 1.1.1.1) 5 [valid
1 W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(F)XG
314: VTGRT WKGTAFGG WKSVE

A33419 ck: 6584 len: 373 | alcohol dehydrogenase (EC 1.1.1.1) class II
1 W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(F)XG
313: VTGRT WKGTAFGG WKSVE

BERTA ck: 6609 len: 373 | alcohol dehydrogenase (EC 1.1.1.1) 2 - rat
1 W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(F)XG
313: VTGRT WKGTAFGG WKSVE

A56643 ck: 1156 len: 374 | alcohol dehydrogenase (EC 1.1.1.1) 2 - mouse
1 W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(F)XG
314: VTGRT WKGTAFGG WKSVE

S68061 ck: 5507 len: 373 | alcohol dehydrogenase (EC 1.1.1.1) class II
1 W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(F)XG
313: VTGRT WKGTAFGG WKSVE

JC4967 ck: 6805 len: 376 | alcohol dehydrogenase (EC 1.1.1.1) class II
1 W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(F)XG
316: VTGRT WKGTAFGG WKSVE

S51187 ck: 4299 len: 376 | alcohol dehydrogenase (EC 1.1.1.1) class II
1 W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(F)XG
316: VTGRT WKGTAFGG WKSVE

A49662 ck: 6276 len: 378 | alcohol dehydrogenase (EC 1.1.1.1) class II
1 W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(F)XG
316: VTGRT WKGTAFGG WKSVE

S51357 ck: 1032 len: 379 | alcohol dehydrogenase (EC 1.1.1.1) Fdh - fr
1 W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(F)XG
319: VTGRT WKGTAFGG WKSVE

S71244 ck: 5257 len: 379 | alcohol dehydrogenase (EC 1.1.1.1) class II
1 W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(F)XG
317: VTGRT WKGTAFGG WKSVE
```

```
D64763 ck: 7661 len: 369 | alcohol dehydrogenase (EC 1.1.1.1) C - Esc
1 W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(F)XG
309: VTGRT WKGSAPFG VKGRS

S57525 ck: 7402 len: 369 | alcohol dehydrogenase (EC 1.1.1.1) C - Esc
1 W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(F)XG
309: VTGRT WKGSAPFG VKGRT

H64052 ck: 2043 len: 378 | alcohol dehydrogenase (EC 1.1.1.1) HI0185 -
1 W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(F)XG
318: VTGRT WKGSAPFG VKGRS

S31140 ck: 583 len: 386 | alcohol dehydrogenase (EC 1.1.1.1) SFA1 -
1 W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(F)XG
322: VTGRT WKGSAPFG IKGRS

JN0447 ck: 8341 len: 381 | alcohol dehydrogenase (EC 1.1.1.1) PDH1 -
1 W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(F)XG
320: VTGRT WKGAAPFG VKGRS

B54075 ck: 7421 len: 663 | arachidonate 12-lipoxygenase (EC 1.13.11.3)
1 W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(F)XG
223: RVRNS WKEDAPFG YQFLN

S30051 ck: 6102 len: 663 | arachidonate 12-lipoxygenase (EC 1.13.11.3)
1 W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(F)XG
223: RVRNS WKEDAPFG YQFLN

I38344 ck: 431 len: 26,926 | titin, cardiac muscle [validated] - human
1 W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(Y)XG
18,126: NVTIK WKGPAYDG GSKIT

NCECX5 ck: 1854 len: 1,180 | exodeoxyribonuclease V (EC 3.1.11.5) 135K c
1 W(K,R)XX(S,A)(Y,F)XG
W(R)XX(S)(Y)XG
901: LPGDN WRVTSYSG LQORG

A35742 ck: 2790 len: 513 | aqualysin (EC 3.4.21.-) I precursor - Ther
1 W(K,R)XX(S,A)(Y,F)XG
W(R)XX(A)(Y)XG
495: AGIYL WRIYAYSG SGMYE

S33643 ck: 8565 len: 733 | transforming protein B-myb - African clawed
```

[illegible]

S20901 ck: 1434 len: 6,805 | titin - rabbit (fragment)  
1 W(K,R)XX(S,A)(Y,F)XG  
6,485: NVTLK WKKPAVDG GSKIT

E91088 ck: 2018 len: 1,180 | DNA helicase RecB [imported] - Escherichia  
1 W(K,R)XX(S,A)(Y,F)XG  
901: LPGDN WVRTSYSG LQORG

B82091 ck: 9551 len: 1,208 | exodeoxyribonuclease V, 135 kDa chain VC232  
1 W(K,R)XX(S,A)(Y,F)XG  
906: AIDRR WVRTSYSG LVMQS

G85933 ck: 2018 len: 1,180 | DNA helicase RecB [imported] - Escherichia  
1 W(K,R)XX(S,A)(Y,F)XG  
901: LPGDN WVRTSYSG LQORG

AD0125 ck: 4557 len: 1,220 | exodeoxyribonuclease V (EC 3.1.11.5) beta d  
1 W(K,R)XX(S,A)(Y,F)XG  
904: KQODY WVRTSYSG LQORG

AB0865 ck: 4255 len: 1,181 | exonuclease V chain [imported] - Salmonella  
1 W(K,R)XX(S,A)(Y,F)XG  
901: LLYDS WVRTSYSG LQORG

T16557 ck: 2841 len: 551 | hypothetical protein K04E7.3 - Caenorhabditis  
1 W(K,R)XX(S,A)(Y,F)XG  
376: RADYS WRN1SYSG SSDCY

S41178 ck: 957 len: 159 | gene 36 protein - phage SPPI  
1 W(K,R)XX(S,A)(Y,F)XG  
77: GVSQS WRTGAPEG QDGKR

H64449 ck: 6435 len: 70 | ribosomal protein L24E - Methanococcus jann  
1 W(K,R)XX(S,A)(Y,F)XG  
4: MPE WRTCSFCG YEIEP

S23164 ck: 5378 len: 65 | light-harvesting protein alpha chain - Ectocarpus  
1 W(K,R)XX(S,A)(Y,F)XG  
58: ENPGI WKRTSYDG

A9285 ck: 5165 len: 422 | hypothetical protein nodC-like [imported]  
1 W(K,R)XX(S,A)(Y,F)XG

415: YGVSE W(R)XX(S)(Y)XG  
WRGSSYLK

D70475 ck: 5280 len: 392 | conserved hypothetical protein aq\_2044 - Agrobacterium  
1 W(K,R)XX(S,A)(Y,F)XG  
127: YVSYN WKRSPFEG KDFED

E72167 ck: 405 len: 146 | A32L protein - variola minor virus (strain  
1 W(K,R)XX(S,A)(Y,F)XG  
73: DVKQK WRCVAYPG NGFVS

JQ1834 ck: 405 len: 146 | 3L protein - variola major virus  
1 W(K,R)XX(S,A)(Y,F)XG  
73: DVKQK WRCVAYPG NGFVS

S46858 ck: 405 len: 146 | A31L protein - variola virus  
1 W(K,R)XX(S,A)(Y,F)XG  
73: DVKQK WRCVAYPG NGFVS

H90733 ck: 8757 len: 199 | probable tail assembly protein [imported] -  
1 W(K,R)XX(S,A)(Y,F)XG  
180: WRHRA WRASFTG ICNDL

F90834 ck: 2142 len: 247 | tail assembly protein [imported] - Escherichia  
1 W(K,R)XX(S,A)(Y,F)XG  
228: WRHRA WRASFTG ICNDL

B85584 ck: 3865 len: 224 | probable tail component of prophage CP-933K  
1 W(K,R)XX(S,A)(Y,F)XG  
205: WRHRA WRASFTG ICNDL

A98950 ck: 7492 len: 261 | hypothetical protein ECs2569 [imported] - E. coli  
1 W(K,R)XX(S,A)(Y,F)XG  
28: GSFV WRMSYFG DTLAH

F82120 ck: 3098 len: 260 | zinc ABC transporter, permease protein VC20  
1 W(K,R)XX(S,A)(Y,F)XG  
28: GSFV WRMSYFG DTLAH

F82959 ck: 5958 len: 262 | permease of ABC zinc transporter ZnuB PA550  
1 W(K,R)XX(S,A)(Y,F)XG  
28: GSFV WRMSYFG DTLSH

1 A64066 ck: 1426 len: 261 ! probable membrane protein HI0407 - Haemophilus influenzae  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(A)(F)XG  
28: GVFVV WRRMAYFG DTLSH

1 E85798 ck: 7492 len: 261 ! hypothetical protein yebI [imported] - Escherichia coli  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(S)(Y)XG  
28: GSFVV WRRMSYFG DTLAH

1 AC0251 ck: 7586 len: 261 ! high-affinity zinc uptake system membrane protein P1 - Escherichia coli  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(S)(Y)XG  
28: GSFVV WRRMSYFG DTLAH

1 AF3531 ck: 8470 len: 284 ! high-affinity zinc uptake system membrane protein P1 - Escherichia coli  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(A)(Y)XG  
40: GCFII WRRMAYFG DTMAH

1 C64948 ck: 7831 len: 261 ! probable membrane protein yebI - Escherichia coli  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(S)(Y)XG  
28: GSFVV WRRMSYFG DTLAH

1 AF2763 ck: 9687 len: 272 ! hypothetical protein znuB [imported] - Agrobacterium tumefaciens  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(A)(Y)XG  
29: GCFVV WRRMAYFG DTMAH

1 AI0742 ck: 7341 len: 261 ! high-affinity zinc uptake system membrane protein P1 - Escherichia coli  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(S)(Y)XG  
28: GSFVV WRRMSYFG DTLAH

1 B97544 ck: 5850 len: 298 ! permease of ABC zinc transporter znuB (PASA) - Agrobacterium tumefaciens  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(A)(Y)XG  
55: GCFVV WRRMAYFG DTMAH

1 S65290 ck: 8779 len: 475 ! clathrin-associated protein complex medium 1 - Escherichia coli  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(S)(F)XG  
382: KSAIL WKIRSFPG GKEYS

1 C96633 ck: 2687 len: 428 ! probable Serine/Threonine protein kinase P8 - Escherichia coli  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(S)(F)XG  
346: KDALV WKIKSFPG NKEYM

1 D70786 ck: 6149 len: 379 ! probable gcvT protein - Mycobacterium tuberculosis  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(S)(Y)XG

1 W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(A)(F)XG  
275: GMAVG WRKDAFFG RAALL

1 T44888 ck: 3832 len: 367 ! probable aminomethyltransferase (EC 2.1.2.1) - Escherichia coli  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(A)(F)XG  
263: GMAIG WRKDAFLG RDALL

1 A39484 ck: 2015 len: 280 ! androgen-withdrawal apoptosis protein RVPI1 - Escherichia coli  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(A)(F)XG  
29: CALPM WRVSAFIG SSIIT

1 T32510 ck: 5742 len: 246 ! hypothetical protein C44B12.3 - Caenorhabditis elegans  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(S)(Y)XG  
87: VVKMT WKQSYDG VLAFV

1 T00479 ck: 1756 len: 303 ! probable phosphatidylinositol-glycan synthase 1 - Escherichia coli  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(A)(Y)XG  
15: IPGPK WRKVAYG MQIGY

1 A56152 ck: 5845 len: 213 ! major 25k outer membrane protein precursor - Escherichia coli  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(A)(F)XG  
74: IKPDD WKAGAFAG WNFOQ

1 AC3408 ck: 5809 len: 213 ! 25K outer-membrane immunogenic protein precursor - Escherichia coli  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(A)(F)XG  
74: IKPDD WKAGAFAG WNFOQ

1 G85506 ck: 391 len: 198 ! hypothetical protein 20246 [imported] - Escherichia coli  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(A)(F)XG  
48: VTPPQ WRNKAFNG LKDPE

1 F90655 ck: 6047 len: 215 ! hypothetical protein ECs0214 [imported] - Escherichia coli  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(A)(F)XG  
65: VTPPQ WRNKAFNG LKDPE

1 G90978 ck: 8152 len: 227 ! hypothetical protein ECs2799 [imported] - Escherichia coli  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(S)(Y)XG  
35: DEIKY WRTSYKG GKLPE

1 AF0118 ck: 8384 len: 765 ! probable kinase YPO0966 [imported] - Yersinia enterocolitica  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(S)(Y)XG  
306: ADAPL WRTISYPG GKGVV

```

1 AG0179 ck: 7342 len: 766 | hypothetical protein YP01473 [imported] - Y
W(K,R)XX(S,A)(Y,F)XG
W(R)XX(S)(F)XG
306: ADAPL WRTISYFG GKGVV
1 AG0697 ck: 4455 len: 122 | probable pathogenicity island protein STY17
W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(F)XG
70: KALAN WKPAAFQG IPQRL
1 F87390 ck: 9243 len: 613 | TonB-dependent receptor, probable [imported]
W(K,R)XX(S,A)(Y,F)XG
W(R)XX(A)(Y)XG
370: KGDTH WRAAYAG FRPPT
1 S60618 ck: 760 len: 441 | 4-alpha-glucanotransferase (EC 2.4.1.25) -
W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(Y)XG
348: EGQTF WKWPAYNG PPSGI
1 F83354 ck: 8784 len: 538 | probable sulfatase PA2333 [imported] - Pseu
W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(Y)XG
455: VRSER WKYIAYDG FRAQL
1 S78561 ck: 548 len: 937 | CS3 pilin synthesis protein, 104K - Bacheri
W(K,R)XX(S,A)(Y,F)XG
W(R)XX(A)(F)XG
595: SIETD WGRAPFG YLSPY
1 H75258 ck: 3668 len: 206 | probable 3-demethylubiquinone-9 3-methyltra
W(K,R)XX(S,A)(Y,F)XG
W(R)XX(S)(F)XG
111: VEETG WRTASPDG VVGA
1 T34972 ck: 1160 len: 330 | probable membrane protein - Streptomyces co
W(K,R)XX(S,A)(Y,F)XG
W(R)XX(A)(F)XG
31: KARLR WRLAPAG FVGVV
1 T06088 ck: 7947 len: 700 | hypothetical protein T9A14.170 - Arabidopsi
W(K,R)XX(S,A)(Y,F)XG
W(R)XX(S)(Y)XG
645: PQQIN WRPPSYFG RDDLE
1 T02995 ck: 2338 len: 530 | unspecific monooxygenase (EC 1.14.14.1) -
W(K,R)XX(S,A)(Y,F)XG
W(R)XX(A)(F)XG
254: RGCSP WRDPAPVG GNDYY
1 T00208 ck: 8858 len: 777 | transposase-like protein - fungus (Fusarium

```

```

1 W(K,R)XX(S,A)(Y,F)XG
W(R)XX(S)(F)XG
402: ERFEI WRKQSFHG KLHNF
1 A56236 ck: 8890 len: 1,220 | probable RNA helicase 1 - human
W(K,R)XX(S,A)(Y,F)XG
W(K)XX(A)(F)XG
538: NDIPE WKGHAFGG NKASY
1 S54293 ck: 5936 len: 1,083 | regulator protein p122-RhoGAP - rat
W(K,R)XX(S,A)(Y,F)XG
W(R)XX(S)(F)XG
393: NSSVN WRTGSFHG PGHLS
1 H71119 ck: 9251 len: 278 | hypothetical protein PH0727 - Pyrococcus hc
W(K,R)XX(S,A)(Y,F)XG
W(R)XX(S)(Y)XG
99: PERVG WRVSSYMG ISFQN
1 G59435 ck: 9802 len: 1,091 | DLC-1 (deleted in liver cancer), p122 [impo
W(K,R)XX(S,A)(Y,F)XG
W(R)XX(S)(F)XG
401: NGSVN WRTGSFHG PGHIS

```

Databases searched:  
 NBRF, Release 76.1, Released on 12May2003, Formatted on 10Jun2003

Total finds: 98  
 Total length: 96,168,682  
 Total sequences: 283,308  
 CPU time: 02:12.67

```
! FINDPATTERNS on-swp:* allowing 0 mismatches
!
! 1 W(K,R)XX(S,A) (Y,F)XG
January 12, 2004 10:19 ..
ADH3_ECOLI ck: 7661 len: 369 ! P25437 escherichia coli. alcohol dehydrogen
1 W(K,R)XX(S,A) (Y,F)XG
W(K)xx(A) (F)XG
309: VTGRV WKGSAFPG VKGRS
ADH3_HAEIN ck: 2043 len: 378 ! P44557 haemophilus influenzae. putative alcoh
1 W(K,R)XX(S,A) (Y,F)XG
W(K)xx(A) (F)XG
318: VTGRV WKGSAFPG VKGRS
ADH3_PASPI ck: 798 len: 369 ! P39450 pasteurella piscicida (photobacteriu
1 W(K,R)XX(S,A) (Y,F)XG
W(K)xx(A) (F)XG
309: VTGRV WKGTAFFG VKGRT
ADH1_GADMO ck: 1925 len: 375 ! P81600 gadus morhua (atlantic cod). alcohol
1 W(K,R)XX(S,A) (Y,F)XG
W(K)xx(A) (F)XG
315: VTGRV WKATAFPG WKSVE
ADH1_RHOSH ck: 2905 len: 376 ! P72324 rhodobacter sphaeroides (rhodospseud
1 W(K,R)XX(S,A) (Y,F)XG
W(K)xx(A) (F)XG
316: VTGRV WKGSAFPG ARGRT
ADH1_GADMO ck: 1722 len: 375 ! P81601 gadus morhua (atlantic cod). alcohol
1 W(K,R)XX(S,A) (Y,F)XG
W(K)xx(A) (F)XG
315: VTGRV WKGTAFFG YKSVE
ADH1_ARATH ck: 5269 len: 379 ! Q96533 arabidopsis thaliana (mouse-ear cree
1 W(K,R)XX(S,A) (Y,F)XG
W(K)xx(A) (F)XG
317: VTGRV WKGTAFFG PKSRT
ADH1_CABEL ck: 9402 len: 384 ! Q17335 caenorhabditis elegans. alcohol dehy
1 W(K,R)XX(S,A) (Y,F)XG
W(K)xx(A) (F)XG
321: VTGRV WKGTAFFG WKSVE
ADH1_PROME ck: 8245 len: 378 ! P46415 drosophila melanogaster (fruit fly).
1 W(K,R)XX(S,A) (Y,F)XG
W(K)xx(A) (F)XG
318: VTGRV WKGSAFPG WRSVS
ADH1_HORSE ck: 6584 len: 373 ! P19854 equus caballus (horse). alcohol dehy
1 W(K,R)XX(S,A) (Y,F)XG
W(K)xx(A) (F)XG
313: VTGRV WKGTAFFG WKSVE
ADH1_UROHA ck: 5507 len: 373 ! P80467 uromastix hardwickii (indian spiny-t:
ADH1_HUMAN ck: 6689 len: 373 ! P11766 homo sapiens (human). alcohol dehydr
1 W(K,R)XX(S,A) (Y,F)XG
W(K)xx(A) (F)XG
313: VTGRV WKGTAFFG WKSVE
ADH1_MAIZE ck: 4477 len: 381 ! P93629 zea mays (maize). alcohol dehydrogen
1 W(K,R)XX(S,A) (Y,F)XG
W(K)xx(A) (F)XG
319: VTGRV WKGTAFFG FKGRS
ADH1_MOUSE ck: 8619 len: 373 ! P28474 mus musculus (mouse). alcohol dehydr
1 W(K,R)XX(S,A) (Y,F)XG
W(K)xx(A) (F)XG
313: VTGRV WKGTAFFG WKSVE
ADH1_MYXGL ck: 4299 len: 376 ! P80360 myxine glutinosa (atlantic hagfish).
1 W(K,R)XX(S,A) (Y,F)XG
W(K)xx(A) (F)XG
316: VTGRV WKGAAFFG WKSVE
ADH1_OCTVU ck: 6276 len: 378 ! P81431 octopus vulgaris (octopus). alcohol
1 W(K,R)XX(S,A) (Y,F)XG
W(K)xx(A) (F)XG
316: VTGRV WKGTAFFG FKSRD
ADH1_ORYSA ck: 4843 len: 381 ! P93436 oryza sativa (rice). alcohol dehydro
1 W(K,R)XX(S,A) (Y,F)XG
W(K)xx(A) (F)XG
319: VTGRV WKGTAFFG FKSRs
ADH1_PEA ck: 405 len: 378 ! P80572 pisum sativum (garden pea). alcohol
1 W(K,R)XX(S,A) (Y,F)XG
W(K)xx(A) (F)XG
316: VTGRV WKGTAFFG FKSRs
ADH1_RABIT ck: 5825 len: 373 ! O19053 oryctolagus cuniculus (rabbit). alco
1 W(K,R)XX(S,A) (Y,F)XG
W(K)xx(A) (F)XG
313: VTGRV WKGTAFFG WKSVE
ADH1_RAT ck: 6609 len: 373 ! P12711 rattus norvegicus (rat). alcohol dehy
1 W(K,R)XX(S,A) (Y,F)XG
W(K)xx(A) (F)XG
313: VTGRV WKGTAFFG WKSVE
ADH1_SPAAU ck: 6805 len: 376 ! P79896 sparus aurata (gilthead sea bream).
1 W(K,R)XX(S,A) (Y,F)XG
W(K)xx(A) (F)XG
316: VTGRV WKGTAFFG WKSVE
ADH1_UROHA ck: 5507 len: 373 ! P80467 uromastix hardwickii (indian spiny-t:
```





1	LOXL_MOUSE	ck: 3173	len: 662	W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(F)XG WKEDAFPG	1	P39654	mus musculus (mouse)	arachidonate 1	1	401: NGSVN	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(F)XG WRTGSFHG	PGHIS				
1	222: RVRNS															
1	MGTA_THEME	ck: 982	len: 441	W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(Y)XG WKWPAYNG	1	P80099	thermotoga maritima	4-alpha-glucan	1	402: NSSVN	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(F)XG WRTGSFHG	PGHLS				
1	348: EGQTP															
1	MYBB_XENLA	ck: 2650	len: 743	W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(F)XG WKTVAFGG	1	P52551	xenopus laevis (african clawed frog)		1	401: NSSVN	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(F)XG WRTGSFHG	PGHLS				
1	705: PWTAA															
1	OM25_BRUAB	ck: 5845	len: 213	W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(F)XG WKAGAFAG	1	Q44664	brucella abortus	25 kda outer-membr	1	SERA_MYCLE	ck: 421	len: 528	1	O33116	mycobacterium leprae	d-3-phosphogly
1	74: IKPDD									129: LRAHI	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(F)XG WKRSPFSG	TEIFG				
1	OM25_BRUCA	ck: 6016	len: 213	W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(F)XG WKAGAFAG	1	Q45110	brucella canis	25 kda outer-membr	1	SERA_MYCTU	ck: 1055	len: 528	1	O53243	mycobacterium tuberculosis	d-3-phos
1	74: IKPDD									129: LREHT	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(F)XG WKRSPFSG	TEIFG				
1	OM25_BRUME	ck: 5809	len: 213	W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(F)XG WKAGAFAG	1	Q45321	brucella melitensis	25 kda outer-me	1	SPS2_MOUSE	ck: 9022	len: 452	1	P97364	mus musculus (mouse)	selenide,water
1	74: IKPDD									52: GFSPS	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(F)XG WRLTSFSG	MKGCG				
1	OM25_BRUNE	ck: 5851	len: 213	W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(F)XG WKAGAFAG	1	Q45326	brucella neotomae	25 kda outer-memb	1	SSAM_SALTY	ck: 5313	len: 122	1	P74855	salmonella typhimurium	secretion sy
1	74: IKPDD									70: KALAN	W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(F)XG WKPAAFQG	IPQRL				
1	OM25_BRUOV	ck: 2394	len: 201	W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(F)XG WKAGAFAG	1	Q45335	brucella ovis	25 kda outer-membrane	1	STAD_LINUS	ck: 845	len: 396	1	P32062	linum usitatissimum (flax)	(linseed)
1	74: IKPDD									340: FLVGR	W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(F)XG WKVDAFTG	LSGEG				
1	OM25_BRUSU	ck: 5911	len: 213	W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(F)XG WKAGAFAG	1	Q45689	brucella suis	25 kda outer-membrane	1	UPD2_SCHPO	ck: 3117	len: 1,010	1	Q9he05	schizosaccharomyces pombe (fission)	
1	74: IKPDD									706: VFRTI	W(K,R)XX(S,A)(Y,F)XG W(K)XX(A)(Y)XG WKQPAYFG	KLEQE				
1	R24E_METJA	ck: 6435	len: 70	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(F)XG WRTCSFGG	1	P54064	methanococcus jannaschii	50s ribosc	1	VA28_VARV	ck: 405	len: 146	1	P33847	variola virus	protein a28. 10/2001
1	4: MPE									73: DVKQK	W(K,R)XX(S,A)(Y,F)XG W(R)XX(A)(Y)XG WRCVAYPG	NGFVS				
1	RHG7_HUMAN	ck: 9918	len: 1,091	W(K,R)XX(S,A)(Y,F)XG W(R)XX(S)(F)XG WRTCSFGG	1	Q96qb1	homo sapiens (human)	rho-gtpase-act	1	VAT_CAMVC	ck: 3857	len: 159	1	P03549	cauliflower mosaic virus (strain cm-	
										61: SLLGI	W(K,R)XX(S,A)(Y,F)XG W(K)XX(S)(Y)XG WKINSYFG	LSKDP				

1	VAT_CAMVD	ck: 3377	len: 159	! P03550 cauliflower mosaic virus (strain d/h	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	VRGSAFGG	VKGRT	310: VTGRV	ck: 5402	len: 182	! P97158 escherichia coli. 20kd protein. 12/2
1	61: SLLGI	WKINSYFG	LSKDP		1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG						
1	VAT_CAMVE	ck: 3139	len: 159	! Q02966 cauliflower mosaic virus (strain bdc	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG	WKINSYFG	LSKDP	24: SIETD	ck: 7402	len: 369	! Q59399 escherichia coli. formaldehyde dehy
1	61: SLLGI	WKINSYFG	LSKDP		1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG						
1	VAT_CAMVN	ck: 3038	len: 159	! Q00965 cauliflower mosaic virus (strain ny8	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG	WKINSYFG	LSKDP	309: VTGRV	ck: 760	len: 441	! Q60035 thermotoga maritima. 4-alpha-glucan
1	61: SLLGI	WKINSYFG	LSKDP		1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG						
1	VAT_CAMVP	ck: 3023	len: 159	! P19818 cauliflower mosaic virus (strain pvl	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG	WKINSYFG	LSKDP	348: EGQTF	ck: 224	len: 369	! O24687 anabaena azollae. glutathione depend
1	61: SLLGI	WKINSYFG	LSKDP		1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG						
1	VAT_CAMVS	ck: 3030	len: 159	! P03548 cauliflower mosaic virus (strain str	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG	WKINSYFG	LSKDP	309: VTGRV	ck: 2507	len: 285	! Q937q0 salmonella enterica subsp. enterica
1	61: SLLGI	WKINSYFG	LSKDP		1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG						
1	VAT_CAMVW	ck: 8557	len: 99	! Q01087 cauliflower mosaic virus (strain w26	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG	WKINSYFG	LSKDP	196: TMENP	ck: 7330	len: 303	! P97157 escherichia coli. 33kd protein. 12/2
1	61: SLLGI	WKINSYFG	LSKDP		1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG						
1	VTAK_LAMED	ck: 9747	len: 199	! P03729 bacteriophage lambda. tail assembly	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	WRSAFTG	IYNDL	145: SIETD	ck: 9791	len: 431	! Q9f9h3 burkholderia cepacia (pseudomonas ce
1	180: WRHRA	WRSAFTG	IYNDL		1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG						
1	YVD3_CABEL	ck: 2841	len: 551	! P55114 caenorhabditis elegans. hypothetical	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG	WRN1SYSG	SSDCY	414: MRDAT	ck: 6278	len: 369	! Q812e3 proteus vulgaris. alcohol dehydrogen
1	376: RADYS	WRN1SYSG	SSDCY		1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG						
1	ZNUB_ECOLI	ck: 7831	len: 261	! P39832 escherichia coli. high-affinity zinc	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG	WRN1SYSG	SSDCY	309: VTGRV	ck: 1674	len: 1,083	! Q9rph6 mycobacterium smegmatis. recb. 3/200.
1	28: GSFVV	WRN1SYSG	SSDCY		1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG						
1	ZNUB_HABIN	ck: 1426	len: 261	! P44691 haemophilus influenzae. high-affin	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG	WRN1SYSG	SSDCY	766: AIDMA	ck: 4956	len: 369	! Q8gms5 synechococcus sp. (strain pcc 7942)
1	28: GVFVV	WRN1SYSG	SSDCY		1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG						
1	Q9RDU5	ck: 3052	len: 372	! Q9rdu5 pseudomonas sp. putative formaldehyd	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG	WRN1SYSG	SSDCY				

309: VTGRV	WRGSAFGG	VKGRS	Q8TC92	ck: 6092	len: 643	! Q8tc92 homo sapiens (human). hypothetical f
1	Q8X0U5	ck: 9212	len: 380	! Q8x0u5 neurospora crassa. probable alcohol	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG
319: VTGRV	WRGSAFGG	VKGRS	632: TLEKR	WKLCAPEG	IKTT	
1	O74636	ck: 8958	len: 777	! O74636 fusarium oxysporum. transposase-like	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(F)XG	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG
1	402: ERFBI	WRKQSPFG	KLHNF			
1	Q96V39	ck: 6889	len: 380	! Q96v39 pichia angusta (yeast) (hansenula po	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG
1	318: VTGRV	WRGCAFGG	IKGRT			
1	Q8J2V2	ck: 8797	len: 230	! Q8j2v2 gibberella zeae (fusarium graminearu	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(F)XG	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG
1	170: IDTDD	WRYSSPFG	ABPSL			
1	Q8J0F4	ck: 9502	len: 1,173	! Q8j0f4 penicillium citrinum. hmg-coa reduct	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(F)XG	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG
1	97: GPQNG	WKQSFDPG	DADVL			
1	Q8J0F1	ck: 4488	len: 380	! Q8j0f1 candida boidinii (yeast). formaldehy	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG
1	318: VTGRV	WRGCAFGG	VKGRT			
1	Q8WZB3	ck: 404	len: 26,926	! Q8wzb3 homo sapiens (human). n2b-titin isc	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(Y)XG	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG
1	18,126: NVTLK	WKKPAYDG	GSKIT			
1	Q8NFW8	ck: 3639	len: 434	! Q8nfw8 homo sapiens (human). cytidine monop	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(Y)XG	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG
1	365: EMGLC	WKEVAYLG	NEVSD			
1	Q8WZ42	ck: 1298	len: 34,350	! Q8wz42 homo sapiens (human). titin. 3/2003	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(Y)XG	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG
1	25,550: NVTLK	WKKPAYDG	GSKIT			
1	Q8NB11	ck: 587	len: 496	! Q8nb11 homo sapiens (human). hypothetical p	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(Y)XG	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(F)XG
1	4: MAL	WRGSAYAG	FLALA			
1	Q9NJC3	ck: 745	len: 377	! Q9njc3 branchiostoma lanceolatum (common l	W(K,R)XX(S,A)(Y,F)XG	W(K,R)XX(S,A)(Y,F)XG

317: VTGRV	W(K,R)XX(A) (F)XG WKGTAFGG	WKSVD	Q9N356	ck: 7111	len: 317	1	Q9n356 caenorhabditis elegans. hypothetical
Q9BJ33	ck: 1200	len: 377	1	Q9bj33 branchiostoma floridae (florida land	W(K,R)XX(S,A) (Y,F)XG W(K)XX(A) (F)XG WKGTAFGG	W(K,R)XX(S,A) (Y,F)XG W(K)XX(S) (Y)XG WKQKSYDG VLAPF	241: VVRQT
317: VTGRV	W(K,R)XX(S,A) (Y,F)XG W(K)XX(A) (F)XG WKGTAFGG	WKSVE	Q9VA05	ck: 5184	len: 1,431	1	Q9va05 drosophila melanogaster (fruit fly).
Q9NP22	ck: 1806	len: 432	1	Q9np22 plasmodium falciparum. nima-related	W(K,R)XX(S,A) (Y,F)XG W(K)XX(S) (Y)XG WKAISYRG	W(K,R)XX(S,A) (Y,F)XG W(K)XX(S) (F)XG WKNVSPAG GIDNS	318: VVIAT
43: QEPFC	WKAISYRG	LKERE	Q8ISD5	ck: 9049	len: 1,057	1	Q8is5d5 plasmodium falciparum (isolate 3d7).
Q965R0	ck: 8060	len: 554	1	Q965r0 caenorhabditis elegans. hypothetical	W(K,R)XX(S,A) (Y,F)XG W(K)XX(A) (F)XG WKGTAFGG	W(K,R)XX(S,A) (Y,F)XG W(K)XX(S) (Y)XG WKAISYRG LKERE	43: QEPFC
494: VTGRT	WKGTAFGG	WKSVE	Q95K71	ck: 1821	len: 414	1	Q95k71 macaca fascicularis (crab eating mac
Q9BJ34	ck: 835	len: 377	1	Q9bj34 branchiostoma floridae (florida land	W(K,R)XX(S,A) (Y,F)XG W(K)XX(A) (F)XG WKGTAFGG	W(K,R)XX(S,A) (Y,F)XG W(K)XX(A) (F)XG WKLCAFGG IKTT	403: TLEKR
317: VTGRV	W(K,R)XX(S,A) (Y,F)XG W(K)XX(A) (F)XG WKGTAFGG	WKSVE	Q28733	ck: 9453	len: 6,875	1	Q28733 oryctolagus cuniculus (rabbit). titi
Q8WS89	ck: 6358	len: 377	1	Q8ws89 ciona intestinalis. alcohol dehydrog	W(K,R)XX(S,A) (Y,F)XG W(K)XX(A) (F)XG WKGTAFGG	W(K,R)XX(S,A) (Y,F)XG W(K)XX(A) (Y)XG WKKPAYDG GSKIT	6,555: NVTLK
317: VTGRT	WKGTAFGG	YKSVE	Q9B394	ck: 8082	len: 255	1	Q9b394 blackburnia palmarum. cytochrome b (fr
Q18005	ck: 8316	len: 545	1	Q18005 caenorhabditis elegans. hypothetical	W(K,R)XX(S,A) (Y,F)XG W(R)XX(S) (F)XG WRNSPFGG	W(K,R)XX(S,A) (Y,F)XG W(R)XX(S) (F)XG WRQMSFWG ATVIT	85: GYVLP
404: GLVGG	WRNSPFGG	FSNGV	Q9GI47	ck: 9519	len: 348	1	Q9gi47 daphniaphyllum sp. qiu 94162. mataras
Q97363	ck: 7232	len: 313	1	Q97363 bombyx mori (silk moth). lipopolysac	W(K,R)XX(S,A) (Y,F)XG W(K)XX(A) (F)XG WKDVAFIG	W(K,R)XX(S,A) (Y,F)XG W(K)XX(S) (F)XG WKONSFLG HNKNL	77: ISAND
230: MIGSF	WKDVAFIG	FHDWN	Q38144	ck: 957	len: 159	1	Q38144 bacteriophage appl. required for rep
Q961U1	ck: 4884	len: 1,721	1	Q961u1 drosophila melanogaster (fruit fly).	W(K,R)XX(S,A) (Y,F)XG W(R)XX(S) (Y)XG WRPPSYDG	W(K,R)XX(S,A) (Y,F)XG W(R)XX(A) (F)XG WRTGAPEG QDGKR	77: GVSQS
253: SCHLN	WRPPSYDG	GLKVS	Q9B0E2	ck: 7287	len: 412	1	Q9b0e2 staphylococcus aureus temperate phag
Q9NBV9	ck: 7429	len: 327	1	Q9nbv9 manduca sexta (tobacco hawkmoth) (to	W(K,R)XX(S,A) (Y,F)XG W(K)XX(A) (F)XG WKDNAPVG	W(K,R)XX(S,A) (Y,F)XG W(K)XX(S) (F)XG WKNRSEFWG VINNT	35: YDFSP
232: MVGNF	WKDNAPVG	FHDWG	Q8S9Y0	ck: 4807	len: 929	1	Q8s9y0 oryza sativa (japonica cultivar-group
Q9V4F7	ck: 9013	len: 8,971	1	Q9v4f7 drosophila melanogaster (fruit fly).	W(K,R)XX(S,A) (Y,F)XG W(R)XX(S) (Y)XG WRPPSYDG	W(K,R)XX(S,A) (Y,F)XG W(R)XX(A) (Y)XG WRVHAYKG KWNDY	266: KEDCP
7,429: SCHLN	WRPPSYDG	GLKVS	Q8RUM3	ck: 5321	len: 542	1	Q8rum3 oryza sativa (japonica cultivar-group

1	247: FGRPC	W(K,R)XX(S,A)(Y,P)XG W(R)XX(S)(Y)XG WRTLSTQOG	KLFWV	Q9FW81	ck: 4017	len: 1,626	! Q9fw81 oryza sativa (rice). mutator-like tr
1	266: KEDCP	W(K,R)XX(S,A)(Y,P)XG W(R)XX(A)(Y)XG WRVHAYKG	KWNDY	Q8W3H2	ck: 8786	len: 1,638	! Q8w3h2 oryza sativa (rice). mutator-like tr
1	266: KEDCP	W(K,R)XX(S,A)(Y,P)XG W(R)XX(A)(Y)XG WRVHAYKG	KWNDY	Q8LR53	ck: 1421	len: 1,605	! Q8lr53 oryza sativa (japonica cultivar-grou
1	266: KEDCP	W(K,R)XX(S,A)(Y,P)XG W(R)XX(A)(Y)XG WRVHAYKG	KWNDY	Q8LQ12	ck: 4995	len: 1,592	! Q8lq12 oryza sativa (japonica cultivar-grou
1	266: KEDCP	W(K,R)XX(S,A)(Y,P)XG W(R)XX(A)(Y)XG WRVHAYKG	KWNDY	Q9FRA2	ck: 2655	len: 1,011	! Q9fra2 oryza sativa (rice). similar to oryza
1	277: KDGCP	W(K,R)XX(S,A)(Y,P)XG W(R)XX(A)(Y)XG WRVHAYKG	KWKDY	Q947Y7	ck: 3231	len: 2,421	! Q947y7 oryza sativa (rice). putative mutato
1	172: KEDCP	W(K,R)XX(S,A)(Y,P)XG W(R)XX(A)(Y)XG WRVHAYKG	KWNDY	Q94D87	ck: 3033	len: 1,626	! Q94d87 oryza sativa (rice). putative mutato
1	266: KEDCP	W(K,R)XX(S,A)(Y,P)XG W(R)XX(A)(Y)XG WRVHAYKG	KWNDY	Q9AYG3	ck: 3386	len: 1,641	! Q9ayg3 oryza sativa (rice). mutator-like tr
1	266: KEDCP	W(K,R)XX(S,A)(Y,P)XG W(R)XX(A)(Y)XG WRVHAYKG	KWNDY	Q9LDW9	ck: 2865	len: 1,591	! Q9ldw9 oryza sativa (rice). est c28952(c629
1	266: KEDCP	W(K,R)XX(S,A)(Y,P)XG W(R)XX(A)(Y)XG WRVHAYKG	KWNDY	Q8W5M7	ck: 4750	len: 1,597	! Q8w5m7 oryza sativa (rice). putative mutato
1	266: KEDCP	W(K,R)XX(S,A)(Y,P)XG W(R)XX(A)(Y)XG WRVHAYKG	KWNDY	Q94FB8	ck: 695	len: 2,910	! Q94fb8 schizochytrium sp. atcc_20888. poly
1	181: ANFPE	W(K,R)XX(S,A)(Y,P)XG W(R)XX(S)(F)XG WRLDSFEG	PLGNV	064761	ck: 1756	len: 303	! O64761 arabidopsis thaliana (mouse-ear cre

1	266: KEDCP	W(K,R)XX(S,A)(Y,P)XG W(R)XX(A)(Y)XG WRVHAYKG	KWNDY	Q9LDE7	ck: 51	len: 938	! Q9lde7 oryza sativa (rice). est c28952(c629
1	266: KEDCP	W(K,R)XX(S,A)(Y,P)XG W(R)XX(A)(Y)XG WRVHAYKG	KWNDY	Q9FGN6	ck: 275	len: 895	! Q9fgn6 arabidopsis thaliana (mouse-ear cre
1	621: RSQCG	W(K,R)XX(S,A)(Y,P)XG W(R)XX(S)(F)XG WQWSPFAG	LPHFT	Q94LE7	ck: 4734	len: 883	! Q94le7 oryza sativa (rice). putative transf
1	266: KEDCP	W(K,R)XX(S,A)(Y,P)XG W(R)XX(A)(Y)XG WRVHAYKG	VEKYH	Q8SB37	ck: 39	len: 1,656	! Q8sb37 oryza sativa (rice). putative transf
1	266: KEECP	W(K,R)XX(S,A)(Y,P)XG W(R)XX(A)(Y)XG WRVHAYKG	KWNDY	Q9T0J6	ck: 7947	len: 700	! Q9t0j6 arabidopsis thaliana (mouse-ear cre
1	645: PQQIN	W(K,R)XX(S,A)(Y,P)XG W(R)XX(S)(Y)XG WRPPSYFG	RDDLE	Q8S5Y6	ck: 7546	len: 1,557	! Q8s5y6 oryza sativa (japonica cultivar-grou
1	266: KEDCP	W(K,R)XX(S,A)(Y,P)XG W(R)XX(A)(Y)XG WRVHAYKG	KWNDY	Q8S696	ck: 8699	len: 1,530	! Q8s696 oryza sativa (japonica cultivar-grou
1	271: KDGCP	W(K,R)XX(S,A)(Y,P)XG W(R)XX(A)(Y)XG WRVHAYKG	KWKDY	Q8S1F8	ck: 8647	len: 1,080	! Q8s1f8 oryza sativa (japonica cultivar-grou
1	742: AVFDN	W(K,R)XX(S,A)(Y,P)XG W(R)XX(A)(F)XG WRMPAFAG	AGDEQ	O04892	ck: 2338	len: 530	! O04892 nicotiana tabacum (common tobacco).
1	254: RGCSP	W(K,R)XX(S,A)(Y,P)XG W(R)XX(A)(F)XG WRPDAFVG	GNDYY	064761	ck: 1756	len: 303	! O64761 arabidopsis thaliana (mouse-ear cre

1 15: IPGPK W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(A)(Y)XG MQIGY  
Q9LDA3 ck: 5721 len: 1,281 ! Q91da3 oryza sativa (rice). est c28952(c629  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(A)(Y)XG  
237: KEDCP WRVHAYKG KWN DY  
Q8LSZ5 ck: 7458 len: 602 ! Q81sz5 physcomitrella patens (moss). ferred  
W(K,R)XX(S,A)(Y,F)XG  
W(K)xx(S)(F)XG  
394: LIDPS WKRSFPFG VNPQK  
Q8W062 ck: 1142 len: 1,604 ! Q8w062 oryza sativa (rice), and oryza sativ  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(A)(Y)XG  
266: KEDCP WRVHAYKG KWN DY  
Q82014 ck: 9934 len: 396 ! O82014 linum usitatissimum (flax) (linseed)  
W(K,R)XX(S,A)(Y,F)XG  
W(K)xx(A)(F)XG  
340: FLVGR WKVDAFTG LSGEG  
Q8S521 ck: 6884 len: 198 ! Q8s521 zea mays (maize). d-type cyclin (fza  
W(K,R)XX(S,A)(Y,F)XG  
W(K)xx(A)(Y)XG  
97: AIDWI WKVHAYYG FGPLT  
Q8S211 ck: 4528 len: 1,353 ! Q8s211 oryza sativa (japonica cultivar-grou  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(A)(Y)XG  
265: KEDCP WRVHAYKG KWN DY  
Q94E86 ck: 1244 len: 603 ! Q94e86 oryza sativa (rice). b1045d11.16 prc  
W(K,R)XX(S,A)(Y,F)XG  
W(K)xx(A)(F)XG  
410: QTNLS WKYMAFQG KIYAA  
Q9XE23 ck: 820 len: 955 ! Q9xe23 oryza sativa (rice). est c28952(c629  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(A)(Y)XG  
115: KEDCP WRVHAYKG KWN DY  
Q8LN97 ck: 3122 len: 1,536 ! Q8ln97 oryza sativa (japonica cultivar-grou  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(A)(Y)XG  
266: KEDCP WRVHAYKG KWN DY  
Q8LN69 ck: 2184 len: 655 ! Q8ln69 oryza sativa (japonica cultivar-grou  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(A)(Y)XG

266: KEDCP WRVHAYKG KWN DY  
Q8RYT2 ck: 5760 len: 1,110 ! Q8ryt2 oryza sativa (japonica cultivar-grou  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(A)(Y)XG  
209: KEDCP WRVHAYKG KWN DY  
Q9SBA2 ck: 9787 len: 396 ! Q9sba2 linum usitatissimum (flax) (linseed)  
W(K,R)XX(S,A)(Y,F)XG  
W(K)xx(A)(F)XG  
340: FLVGR WKVDAFTG LSGEG  
Q94JG7 ck: 2586 len: 429 ! Q94jg7 oryza sativa (rice), and oryza sativ  
W(K,R)XX(S,A)(Y,F)XG  
W(K)xx(S)(P)XG  
347: RDMV WKVKSFPFG GKDYM  
O22715 ck: 2687 len: 428 ! O22715 arabidopsis thaliana (mouse-ear cres  
W(K,R)XX(S,A)(Y,F)XG  
W(K)xx(S)(F)XG  
346: KDALV WKIKSFPFG NKEYM  
Q9SW79 ck: 8565 len: 274 ! Q9sw79 triticum aestivum (wheat). alternati  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(S)(Y)XG  
21: GRRRR WRISSYWG IEQSK  
Q8H904 ck: 6567 len: 1,597 ! Q8h904 oryza sativa (japonica cultivar-grou  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(A)(Y)XG  
266: KEDCP WRVHAYKG KWN DY  
Q8H8E2 ck: 1340 len: 779 ! Q8h8e2 oryza sativa (japonica cultivar-grou  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(A)(Y)XG  
266: KEDCP WRVHAYKG KWN DY  
Q8H7V5 ck: 7087 len: 1,596 ! Q8h7v5 oryza sativa (japonica cultivar-grou  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(A)(Y)XG  
277: KDGP WRVHAYKG KWKDY  
Q8H5S9 ck: 5613 len: 1,179 ! Q8h5s9 oryza sativa (japonica cultivar-grou  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(A)(Y)XG  
273: KDGP WRVHAYKG KWKDY  
Q8H525 ck: 8356 len: 1,727 ! Q8h525 oryza sativa (japonica cultivar-grou  
W(K,R)XX(S,A)(Y,F)XG  
W(R)xx(A)(Y)XG  
266: KEDCP WRVHAYKG KWN DY

1 Q8H4Y6 ck: 2309 len: 268 ! Q8h4y6 oryza sativa (japonica cultivar-group)  
W(K,R)XX(S,A)(Y,F)XG  
W(R)XX(S)(F)XG  
243: PFRSP WRAVSFG ARRSV

1 Q8H2L9 ck: 9400 len: 1,662 ! Q8h2l9 oryza sativa (japonica cultivar-group)  
W(K,R)XX(S,A)(Y,F)XG  
W(R)XX(A)(Y)XG  
266: KEDCP WRVHAYKG KWNDY

1 Q8H2L7 ck: 8873 len: 1,753 ! Q8h2l7 oryza sativa (japonica cultivar-group)  
W(K,R)XX(S,A)(Y,F)XG  
W(R)XX(A)(Y)XG  
266: KEDCP WRVHAYKG KWNDY

1 Q8GX38 ck: 3045 len: 265 ! Q8gx38 arabidopsis thaliana (mouse-ear cre  
W(K,R)XX(S,A)(Y,F)XG  
W(R)XX(S)(Y)XG  
210: PQQIN WRPPSYFG RDDLE

1 Q8GRQ7 ck: 3759 len: 903 ! Q8grq7 oryza sativa (japonica cultivar-group)  
W(K,R)XX(S,A)(Y,F)XG  
W(R)XX(A)(Y)XG  
266: KSECP WRVHAYKG KWNDY

1 Q88719 ck: 9067 len: 432 ! Q88719 mus musculus (mouse). cmp-n-acetylne  
W(K,R)XX(S,A)(Y,F)XG  
W(K)XX(A)(Y)XG  
363: EMGLC WKEVAYLG NEVSD

1 Q8RSB1 ck: 3258 len: 490 ! Q8rsb1 mus musculus (mouse). similar to hyp  
W(K,R)XX(S,A)(Y,F)XG  
W(K)XX(A)(Y)XG  
198: QKQPA WKVGAYKG KQAIS

1 Q8K2G7 ck: 8878 len: 432 ! Q8k2g7 mus musculus (mouse). cytidine monoph  
W(K,R)XX(S,A)(Y,F)XG  
W(K)XX(A)(Y)XG  
363: EMGLC WKEVAYLG NEVSD

1 Q99KK2 ck: 2584 len: 166 ! Q99kk2 mus musculus (mouse). similar to cyto  
W(K,R)XX(S,A)(Y,F)XG  
W(K)XX(A)(Y)XG  
97: EMGLC WKEVAYLG NEVSD

1 Q9JHG0 ck: 2510 len: 137 ! Q9jhg0 mus musculus (mouse). cbln3. 6/2001  
W(K,R)XX(S,A)(Y,F)XG  
W(K)XX(S)(F)XG  
184: NLILGG WKYSFSG FLIFP

1 Q8C662 ck: 221 len: 374 ! Q8c662 mus musculus (mouse). alcohol dehydro  
W(K,R)XX(S,A)(Y,F)XG

314: VTGRT W(K)XX(A)(F)XG  
WKGTAFGG WKSVE

1 Q8C330 ck: 6000 len: 200 ! Q8c330 mus musculus (mouse). cytidine monoph  
W(K,R)XX(S,A)(Y,F)XG  
W(K)XX(A)(Y)XG  
131: EMGLC WKEVAYLG NEVSD

1 Q8BY11 ck: 241 len: 305 ! Q8by11 mus musculus (mouse). putative hiv-1  
W(K,R)XX(S,A)(Y,F)XG  
W(K)XX(A)(Y)XG  
198: QKQPA WKVGAYKG KQAIS

1 Q8BXA6 ck: 890 len: 224 ! Q8bxa6 mus musculus (mouse). similar to chr  
W(K,R)XX(S,A)(Y,F)XG  
W(R)XX(A)(F)XG  
30: TLLPQ WRVSAFIG SNIIL

1 Q8BWI1 ck: 675 len: 689 ! Q8bwy1 mus musculus (mouse). hypothetical  
W(K,R)XX(S,A)(Y,F)XG  
W(K)XX(S)(Y)XG  
384: QLNNEN WKRHSYAG EQPET

1 Q8BJ63 ck: 3056 len: 490 ! Q8bj63 mus musculus (mouse). putative hiv-1  
W(K,R)XX(S,A)(Y,F)XG  
W(K)XX(A)(Y)XG  
198: QKQPA WKVGAYKG KQAIS

1 Q8BJ58 ck: 6723 len: 398 ! Q8bj58 mus musculus (mouse). putative hiv-1  
W(K,R)XX(S,A)(Y,F)XG  
W(K)XX(A)(Y)XG  
198: QKQPA WKVGAYKG KQAIS

1 Q8BJ31 ck: 3487 len: 307 ! Q8bj31 mus musculus (mouse). putative hiv-1  
W(K,R)XX(S,A)(Y,F)XG  
W(K)XX(A)(Y)XG  
198: QKQPA WKVGAYKG KQAIS

1 Q8BI12 ck: 3107 len: 490 ! Q8bi12 mus musculus (mouse). putative hiv-1  
W(K,R)XX(S,A)(Y,F)XG  
W(K)XX(A)(Y)XG  
198: QKQPA WKVGAYKG KQAIS

1 Q8BHR2 ck: 4917 len: 643 ! Q8bhr2 mus musculus (mouse). hypothetical  
W(K,R)XX(S,A)(Y,F)XG  
W(K)XX(A)(F)XG  
632: TLEKR WKLCAFEG IKTT

1 Q91TT0 ck: 2878 len: 138 ! Q91tt0 tupaia herpesvirus. t22.9. 10/2002  
W(K,R)XX(S,A)(Y,F)XG  
W(R)XX(S)(F)XG  
67: TSVPV WRLCSFGG GFVLG

1	Q8V715	ck: 8144	len: 547	! Q8v715 swine calicivirus. capsid protein. 6	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(Y)XG	73: DVKQK WRCVAYPG	NGFVS		
	410: QDPNQ	WRLPAYGG	ALTNN							
1	Q8QNH4	ck: 1050	len: 284	! Q8qnh4 ectocarpus siliculosus virus. esv-1-	1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG	Q90XR4	ck: 7881	len: 210	! Q90xr4 brachydanio rerio (zebrafish) (danio)
	75: NCLKN	WKPRFLG	SGAHG				27: CALPM WKVTAFIG	TNIVV		
1	Q9QQN6	ck: 7259	len: 479	! Q9qqn6 sugarcane yellow leaf virus. putativ	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(Y)XG	Q90XR8	ck: 4395	len: 215	! Q90xr8 brachydanio rerio (zebrafish) (danio)
	129: ANLAG	WRAYAYSG	CTISN				30: CALPM WKVTAFIG	ANIVT		
1	Q66159	ck: 2936	len: 159	! Q66159 cauliflower mosaic virus. orf ii. 6/	1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG	Q90XR0	ck: 4854	len: 214	! Q90xr0 brachydanio rerio (zebrafish) (danio)
	61: SLLGI	WKINSYFG	LSKDP				29: CALPM WRVSAFVG	ANIVT		
1	Q83166	ck: 3141	len: 159	! Q83166 cauliflower mosaic virus. aphid tran	1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG	Q90XR9	ck: 2537	len: 209	! Q90xr9 brachydanio rerio (zebrafish) (danio)
	61: SLLGI	WKINSYFG	LSKDP				30: CALPM WKVTAFIG	ANIVT		
1	Q83179	ck: 3686	len: 159	! Q83179 cauliflower mosaic virus. orf ii pro	1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG	Q9DE12	ck: 435	len: 214	! Q9de12 xenopus laevis (african clawed frog)
	61: SLLGI	WKINSYFG	LSKDP				30: CALPM WRVTAFIG	NNIVV		
1	Q9JH75	ck: 3583	len: 479	! Q9jh75 sugarcane yellow leaf virus. putativ	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(Y)XG	Q90XR6	ck: 1235	len: 211	! Q90xr6 brachydanio rerio (zebrafish) (danio)
	129: ANLAG	WRAYAYSG	CTISN				30: IAIPO WKTSAFIG	QNIIT		
1	Q9WI33	ck: 2997	len: 159	! Q9wi33 cauliflower mosaic virus. aphid tran	1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG	Q90XR2	ck: 5577	len: 218	! Q90xr2 brachydanio rerio (zebrafish) (danio)
	61: SLLGI	WKINSYFG	LSKDP				30: CALPM WRVTAFIG	TNIVT		
1	Q83157	ck: 8743	len: 64	! Q83157 cauliflower mosaic virus. aphid acqu	1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG	Q90XD4	ck: 5678	len: 376	! Q90xd4 brachydanio rerio (zebrafish) (danio)
	7: SLLGI	WKINSYFG	LSKDP				316: VTGRT WKGTAFIG	WKSVE		
1	Q83162	ck: 8680	len: 99	! Q83162 cauliflower mosaic virus. hypothetic	1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG	Q90XQ9	ck: 100	len: 214	! Q90xq9 xenopus laevis (african clawed frog)
	61: SLLGI	WKINSYFG	LSKDP				30: CAMP WRVTAFIG	NNIVV		
1	Q8V2M7	ck: 663	len: 146	! Q8v2m7 camelpox virus (strain cp-1). hypoth	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	Q98SR2	ck: 3404	len: 214	! Q98sr2 gallus gallus (chicken). claudin-3. :
							29: CALPM WRVTAFIG	NNIVT		

1	Q90XQ8	ck: 8089	len: 210	! Q90xq8 brachydanio rerio (zebrafish) (danio)	1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG	318: VTGRV	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG	VKGRS
30: TAMAE				DNIIT					
1	Q8UVX9	ck: 8315	len: 209	! Q8uvx9 torpedo marmorata (marbled electric)	1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(F)XG	455: VRSER	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(Y)XG	FRAQL
90: QSSCA				WQCSFNG					
1	Q90WG6	ck: 4720	len: 432	! Q90wg6 oncorhynchus mykiss (rainbow trout)	1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(Y)XG	310: VTGRV	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	VRGRS
355: DKDLD				WKEVAYMG					
1	Q8JIE6	ck: 8389	len: 1,019	! Q8jie6 gallus gallus (chicken). hira. 3/200	1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(Y)XG	28: GSFVV	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(Y)XG	DTLSH
97: KLIMV				WKEAAYIG					
1	Q8AVG4	ck: 4992	len: 211	! Q8avg4 xenopus laevis (african clawed frog)	1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(F)XG	28: GAFVV	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(Y)XG	DTLAH
30: IAIPO				WKMSSFAG					
1	Q8Q7G3	ck: 8999	len: 861	! Q8q7g3 human immunodeficiency virus 1. env	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG	370: KGDTW	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(Y)XG	FRPPT
777: LASGI				WVRNSYLG					
1	O67832	ck: 5280	len: 392	! O67832 aquifex aeolicus. hypothetical prote	1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(F)XG	309: VTGRV	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG	ARGRT
127: YVSVN				WKGSRFEG					
1	Q9KQB7	ck: 3098	len: 260	! Q9kqb7 vibrio cholerae. zinc abc transporte	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(Y)XG	379: ELLGP	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	AGACT
28: GSFVV				WRRMAYFG					
1	Q9KPP6	ck: 9551	len: 1,208	! Q9kpp6 vibrio cholerae. exodeoxyribonuclea	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG	315: NIEAA	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(F)XG	QTDAA
906: AIDRR				WVRTSYSG					
1	Q9KCG9	ck: 2788	len: 540	! Q9kcg9 bacillus halodurans. d-3-phosphoglyc	1	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG	148: CMDAA	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG	KQORI
141: IKAGE				WKRKAFQG					
1	Q9JRB0	ck: 788	len: 378	! Q9jrb0 neisseria meningitidis (serogroup a)	1	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	Q983F3	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG	Q983f3 rhizobium loti (mesorhizobium loti)

264: RDIKI	WRSVSYIG	LISYP		Q8YTB3	ck: 892	len: 369	1	Q8Ytb3 anabaena sp. (strain pcc 7120). glu	
Q8ZPA8	ck: 2185	len: 372	1	Q8zpa8 salmonella typhimurium. alcohol dehy	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	309: VTGRV	WKSAPFGG	ARGRT
309: VTGRV	WKSAPFGG	VKGRT		Q8XCJ0	ck: 7492	len: 261	1	Q8xcj0 escherichia coli o157:h7. orf, hypot	
Q8ZNV6	ck: 6897	len: 261	1	Q8zmv6 salmonella typhimurium. abc superfam	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG	28: GSFVV	WRRMSYFG	DTLAH
28: GSFVV	WRRMSYFG	DTLAH		Q8X847	ck: 2142	len: 247	1	Q8x847 escherichia coli o157:h7. putative t	
Q8ZN10	ck: 8280	len: 199	1	Q8zn10 salmonella typhimurium. gifsy-1 prop	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	228: WRHRA	WRASAF TG	ICNDL
180: WRHRA	WRASAF TG	ICNDP		Q8X7X8	ck: 6047	len: 215	1	Q8x7x8 escherichia coli o157:h7. hypothetical	
Q8ZMB6	ck: 4862	len: 1,181	1	Q8zmb6 salmonella typhimurium. exonuclease	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG	65: VTDPQ	WRNKA FNG	LKDPE
901: LLYDS	WRVTSYSG	LQORG		Q8X6M9	ck: 2018	len: 1,180	1	Q8x6m9 escherichia coli o157:h7. dna helica	
Q8ZH88	ck: 4557	len: 1,220	1	Q8zh88 yersinia pestis. exodeoxyribonucleas	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG	901: LPQDN	WRVTSYSG	LQORG
904: KMQDY	WRVTSYSG	LQQSG		Q8X5J4	ck: 7697	len: 369	1	Q8x5j4 escherichia coli o157:h7. alcohol de	
Q8ZG44	ck: 7342	len: 766	1	Q8zg44 yersinia pestis. hypothetical protei	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	309: VTGRV	WKSAPFGG	VKGRS
306: ADAPL	WRTISYFG	GKGVV		Q8UF80	ck: 5850	len: 298	1	Q8uf80 agrobacterium tumefaciens (strain c5	
Q8ZG18	ck: 6334	len: 377	1	Q8zgi8 yersinia pestis. probable alcohol de	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	55: GCFVV	WRRMAYFG	DTMAH
310: VTGRV	WKSAPFGG	VKGRS		Q8X3C3	ck: 8152	len: 227	1	Q8x3c3 escherichia coli o157:h7. hypothetical.	
Q8Z6M8	ck: 4455	len: 122	1	Q8z6m8 salmonella typhi. putative pathogeni	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG	35: DEIKY	WRTSYXG	GKLPE
70: KALAN	WKPAAFQG	IPQRL		Q9ACP5	ck: 2721	len: 1,039	1	Q9acp5 streptomyces coelicolor. putative la	
Q8Z5W5	ck: 7341	len: 261	1	Q8z5w5 salmonella typhi. high-affinity zinc	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(Y)XG	603: GGAFA	WKVRAYDG	SAYSA
28: GSFVV	WRRMSYFG	DTLAH		Q9RRD0	ck: 3668	len: 206	1	Q9rrd0 deinococcus radiodurans. 3-demethylu	
Q8Z419	ck: 4255	len: 1,181	1	Q8z419 salmonella typhi. exonuclease v subu	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(F)XG	111: VBETG	WRTASFDG	VVVG A
901: LLYDS	WRVTSYSG	LQORG		Q92P77	ck: 5059	len: 275	1	Q92p77 rhizobium meliloti (sinorhizobium me.	

29: GCFVI	W(R)xx(A)(Y)XG WRRMAYFG	DTMAH	Q8PPF2	ck: 6865	len: 369	! Q8ppf2 xanthomonas axonopodis (pv. citri).
Q8YEQ9	ck: 9722	len: 370	! Q8yeq9 brucella melitensis. alcohol dehydrogenase			
310: VTGRV	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG WKGTAFGG	ARGRT	309: VTGRV	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG WRGSAFGG	VKGRT	
Q8YDJ9	ck: 8470	len: 284	! Q8yjd9 brucella melitensis. high-affinity iron uptake system			
40: GCFII	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(Y)XG WRRMAYFG	DTMAH	Q8PHP1	ck: 333	len: 811	! Q8php1 xanthomonas axonopodis (pv. citri).
Q8YIT4	ck: 3386	len: 368	! Q8yit4 ralstonia solanacearum (pseudomonas)			
308: VTGRE	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG WKGSAFGG	ARGRT	645: ELVAN	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG WRQYAFGG	DLLLT	
Q8XTN7	ck: 4468	len: 368	! Q8xtn7 ralstonia solanacearum (pseudomonas)			
308: VTGRE	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG WKGSAFGG	ARGRT	Q8PA46	ck: 898	len: 205	! Q8pa46 xanthomonas campestris (pv. campestris)
Q8RHM9	ck: 4108	len: 454	! Q8rhm9 fusobacterium nucleatum (subsp. nucleatum)			
226: EIKSN	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(F)XG WKSPSPSG	VLPTE	104: SPNGA	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG WRNAAFQG	YADHM	
Q8REQ9	ck: 5980	len: 303	! Q8req9 fusobacterium nucleatum (subsp. nucleatum)			
216: NIFLS	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(Y)XG WKSIAVAG	FLSSG	Q8P5P2	ck: 6765	len: 369	! Q8p5f2 xanthomonas campestris (pv. campestris)
Q8R8C0	ck: 4513	len: 474	! Q8r8c0 thermoanaerobacter tengcongensis. serine dehydratase			
446: KQGGK	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(Y)XG WKLAAIDG	VYNPV	309: VTGRV	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG WRGSAFGG	VKGRT	
Q8R6S5	ck: 1574	len: 835	! Q8r6s5 thermoanaerobacter tengcongensis. hyaluronate lyase			
608: YGSPT	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG WKDIAFIG	TLNGA	Q8P568	ck: 4077	len: 368	! Q8p568 xanthomonas campestris (pv. campestris)
Q8PPQ7	ck: 6719	len: 697	! Q8ppq7 xanthomonas axonopodis (pv. citri).			
374: PSPDG	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG WKGSAFVG	APSPG	308: VTGRV	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG WRGSAFGG	VKGRS	
Q8PPN3	ck: 2843	len: 368	! Q8ppn3 xanthomonas axonopodis (pv. citri).			
308: VTGRV	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG WRGSAFGG	VKGRS	Q8P541	ck: 7584	len: 697	! Q8p541 xanthomonas campestris (pv. campestris)
			374: PSQDG	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG WKKSAPVG	APAFG	
			Q8P400	ck: 8382	len: 300	! Q8p400 xanthomonas campestris (pv. campestris)
			79: PTPAQ	W(K,R)XX(S,A)(Y,F)XG W(K)xx(A)(F)XG WKQVAFMG	AALLL	
			Q8NWJ8	ck: 6871	len: 412	! Q8nwj8 staphylococcus aureus (strain mw2).



1	28: GSFVV	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG	DTLAH	314: VTGRV	WKSAGFG	VKGRS	
1	Q8FG68	ck: 9474 len: 261	Q8fg68 escherichia coli o6. hypothetical ph	Q8DWE2	ck: 8469 len: 372	Q8dwe2 streptococcus mutans. putative alcohol	
1	71: DEIKY	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG	GEFPE	312: VTGRV	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG WRGSAFGG	VKGKT	
1	904: LPGDN	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG	LQORG	Q8DJN0	ck: 1651 len: 399	Q8djn0 synochococcus elongatus (thermosynoc	
1	Q8F6V8	ck: 4588 len: 1,183	Q8feb3 escherichia coli o6. exodeoxyribonuc	258: HNOVY	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WRNOSYTG	FGMGA	
1	136: VTDFI	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(F)XG	EMANR	32: GSFVV	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(Y)XG WRMAYFG	DTLAH	
1	Q8F4M6	ck: 7773 len: 523	Q8f6v8 leptospira interrogans. putative out	Q8DF77	ck: 391 len: 376	Q8df77 vibrio vulnificus. zn-dependent alco	
1	244: QISSN	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(F)XG WKDPSFEG	SFLPK	315: VTGRV	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG WRGSAFGG	VKGRS	
1	Q8F2V5	ck: 8001 len: 749	Q8f2v5 leptospira interrogans. ribonuclease	Q8DBL8	ck: 5828 len: 1,206	Q8dbl8 vibrio vulnificus. atp-dependent exo	
1	284: LESPI	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(F)XG WRLASPEG	VELKD	909: PIDRL	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WRITSYSG	LVKQG	
1	Q8EYP7	ck: 6380 len: 403	Q8eyp7 leptospira interrogans. argininosucc	Q8D386	ck: 9466 len: 265	Q8d386 wiggleworthia brevialpalpis. yebl pro	
1	149: TIIAP	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(F)XG WRIWSFEG	RSDLI	28: GSFLI	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WRKMSYFG	DTLSH	
1	Q8EXC1	ck: 4765 len: 249	Q8exc1 leptospira interrogans. probable sug	Q8D070	ck: 2620 len: 379	Q8d070 yersinia pestis. alcohol dehydrogena	
1	211: KYMTS	W(K,R)XX(S,A)(Y,F)XG W(K)xx(S)(Y)XG WKSPFSYG	EPRKL	312: VTGRV	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG WRGSAFGG	VKGRS	
1	Q8BFC7	ck: 2100 len: 379	Q8bfc7 shewanella oneidensis. alcohol dehyd	Q8CZY3	ck: 1453 len: 1,241	Q8czy3 yersinia pestis. dna helicase, atp-d	
1	317: VTGRV	W(K,R)XX(S,A)(Y,F)XG W(R)xx(A)(F)XG WRGSAFGG	VKGRS	925: KMQDY	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WRVTSYSG	LQOSG	
1	Q8BF45	ck: 5478 len: 1,259	Q8bf45 shewanella oneidensis. exodeoxyribor	Q8CKW8	ck: 7447 len: 766	Q8ckw8 yersinia pestis. hypothetical. 3/200	
1	949: QYRTP	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WRVGSYSG	LVKNA	306: ADAPL	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WRTISYSG	GKGVV	
1	Q8B800	ck: 4584 len: 376	Q8e800 shewanella oneidensis. zinc-binding	O58458	ck: 9251 len: 278	O58458 pyrococcus horikoshii. hypothetical	
1				99: PERVG	W(K,R)XX(S,A)(Y,F)XG W(R)xx(S)(Y)XG WRVSSYMG	ISFQN	

Q97YM4 ck: 5165 len: 422 ! Q97ym4 sulfolobus solfataricus. n-acetylglu  
 1 W(K,R)XX(S,A)(Y,P)XG  
 W(R)xx(S)(Y)XG  
 415: YGVSE WRGSSYLQ

Q8THB2 ck: 6769 len: 355 ! Q8thb2 methanosarcina acetivorans. iron(iii)  
 1 W(K,R)XX(S,A)(Y,P)XG  
 W(R)xx(A)(P)XG  
 24: PFCLE WRSAPIG FLLLP

Q8Q0X8 ck: 4651 len: 535 ! Q8q0x8 methanosarcina mazei (methanosarcina  
 1 W(K,R)XX(S,A)(Y,P)XG  
 W(K)xx(A)(Y)XG  
 469: QAIEN WKLAAYDG NTGFG

Databases searched:

SWISS-PROT, Release 41.1, Released on 6Jun2003, Formatted on 9Jun2003  
 SPTREMBL, Release 23.0, Released on 4Mar2003, Formatted on 7Mar2003

Total finds: 336  
 Total length: 305,079,309  
 Total sequences: 958,388  
 CPU time: 07:35.08

```

!!AA SEQUENCE 1.0
ID -AAB06419 standard; peptide; 8 AA.
XX
AC AAB06419;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cell adhesion recognition sequence SEQ ID NO: 34.
XX
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PP 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI; 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 39; Page 96; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
SQ Sequence 8 AA;

```

AAB06419 Length: 8 January 12, 2004 11:03 Type: P Check: 2784 ..

1 WKIYSYAG

```

!!AA SEQUENCE 1.0
ID _AAB06420 standard; peptide; 9 AA.
AC AAB06420;
XX
XX 28-SEP-2000 (first entry)
XX
XX Claudin-1 cell adhesion recognition sequence SEQ ID NO: 476.
XX
XX Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.
XX
XX Mammalia.
XX
XX WO200026360-A1.
XX
XX 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-CA01029.
XX
XX 03-NOV-1998; 98US-0185908.
XX 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuck OW, Symonds JM, Gour BJ;
XX
XX WPI; 2000-365610/31.
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX Claim 39; Page 96; 121pp; English.
XX
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
XX Sequence 9 AA;
SQ

```

AAB06420 Length: 9 January 12, 2004 11:03 Type: P Check: 3486 ..

1 WKIYSYAGN

!!AA SEQUENCE 1.0  
ID -AAB06426 standard; peptide; 8 AA.  
XX  
AC AAB06426;  
XX  
DT 28-SEP-2000 (first entry)  
XX  
DE Claudin-1 cell adhesion recognition sequence SEQ ID NO: 485.  
XX  
KW Claudin-1 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection.  
XX  
OS Mammalia.  
XX  
PN WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
PF 03-NOV-1999; 99WO-CA01029.  
XX  
PR 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
PI Blaschuck OW, Symonds JM, Gour BJ;  
XX  
DR WPI; 2000-365610/31.  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
PS Claim 39; Page 96; 121pp; English.  
XX  
CC The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site.  
XX  
SQ Sequence 8 AA;

AAB06426 Length: 8 January 12, 2004 11:03 Type: P Check: 2798 ..

1 WRIYSYAG

!!AA SEQUENCE 1.0  
ID AAB06427 standard; peptide; 9 AA.  
AC AAB06427;  
XX  
DT 28-SEP-2000 (first entry)  
XX  
DE Claudin-1 cell adhesion recognition sequence SEQ ID NO: 486.  
XX  
KW Claudin-1 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection.  
XX  
OS Mammalia.  
XX  
PN WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
PF 03-NOV-1999; 99WO-CA01029.  
XX  
PR 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
PI Blaschuck OW, Symonds JM, Gour BJ;  
XX  
DR WPI; 2000-365610/31.  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
PS Claim 39; Page 96; 121pp; English.  
XX  
CC The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site.  
XX  
SQ Sequence 9 AA;

AAB06427 Length: 9 January 12, 2004 11:03 Type: P Check: 3500 ..

1 WRIYSYAGN

```

!!AA SEQUENCE 1.0
ID _AAB06436 standard; peptide; 10 AA.
XX
AC AAB06436;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 67.
XX
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI; 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 43; Page 96; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 10 AA;

```

AAB06436 Length: 10 January 12, 2004 11:03 Type: P Check: 4153 ..

1 CWKIYSYAGC

```

!!AA SEQUENCE 1.0
ID AAB06445 standard; peptide; 10 AA.
AC AAB06445;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 76.
XX
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI; 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 43; Page 96; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 10 AA;

```

AAB06445 Length: 10 January 12, 2004 11:03 Type: P Check: 4171 ..

1 KWKIYSYAGD

!!AA SEQUENCE 1.0  
ID AAB06454 standard; peptide; 10 AA.  
XX  
AC AAB06454;  
XX  
DT 28-SEP-2000 (first entry)  
XX  
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 85.  
XX  
KW Claudin-1 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection; cyclic.  
XX  
OS Mammalia.  
XX  
PN WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
XX 03-NOV-1999; 99WO-CA01029.  
XX  
PR 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
PI Blaschuck OW, Symonds JM, Gour BJ;  
XX  
DR WPI; 2000-365610/31.  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
PS Claim 43; Page 96; 121pp; English.  
XX  
CC The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site. The present sequence has a cyclic  
CC conformation.  
XX  
SQ Sequence 10 AA;

AAB06454 Length: 10 January 12, 2004 11:03 Type: P Check: 4181 ..

1 KWKIYSYAGE

!!AA SEQUENCE 1.0  
ID AAB06463 standard; peptide; 10 AA.  
AC AAB06463;  
XX 28-SEP-2000 (first entry)  
XX Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 94.  
XX  
XX Claudin-1 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection; cyclic.  
XX  
XX Mammalia.  
OS  
XX  
XX WO200026360-A1.  
PN  
XX  
XX 11-MAY-2000.  
PD  
XX  
XX 03-NOV-1999; 99WO-CA01029.  
PF  
XX  
XX 03-NOV-1998; 98US-0185908.  
PR  
XX 30-MAR-1999; 99US-0282029.  
PR  
XX  
XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
PA  
XX  
XX Blaschuck OW, Symonds JM, Gour BJ;  
PI  
XX  
XX WPI; 2000-365610/31.  
DR  
XX  
XX Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
XX Claim 43; Page 97; 121pp; English.  
PS  
XX  
XX The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site. The present sequence has a cyclic  
CC conformation.  
CC  
XX  
XX Sequence 10 AA;  
SQ

AAB06463 Length: 10 January 12, 2004 11:04 Type: P Check: 4234 ..

1 DWKIYSACK

```

!!AA SEQUENCE 1.0
ID AAB06472 standard; peptide; 10 AA.
XX
AC AAB06472;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 103.
XX
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI; 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 43; Page 97; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 10 AA;

```

AAB06472 Length: 10 January 12, 2004 11:04 Type: P Check: 4235 ..

1 EWKIYSYAGK

!!AA SEQUENCE 1.0  
ID AAB06479 standard; peptide; 8 AA.  
XX  
AC AAB06479;  
XX  
DT 28-SEP-2000 (first entry)  
XX  
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 110.  
XX  
KW Claudin-1 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection; cyclic.  
XX  
OS Mammalia.  
XX  
PN WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
PF 03-NOV-1999; 99WO-CA01029.  
XX  
PR 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
PI Blaschuck OW, Symonds JM, Gour BJ;  
XX  
DR WPI; 2000-365610/31.  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
PS Claim 43; Page 97; 121pp; English.  
XX  
CC The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site. The present sequence has a cyclic  
CC conformation.  
XX  
SQ Sequence 8 AA;  
AAB06479 Length: 8 January 12, 2004 11:04 Type: P Check: 2784 ..  
1 WKIYSYAG

!!AA SEQUENCE 1.0  
 ID AAB06485 standard; peptide; 10 AA.  
 AC AAB06485;  
 DT 28-SEP-2000 (first entry)  
 DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 492.  
 KW Claudin-1 modulating agent; cell adhesion recognition sequence;  
 KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
 KW graft rejection; cyclic.  
 XX  
 OS Mammalia.  
 XX  
 FN WO200026360-A1.  
 XX  
 PD 11-MAY-2000.  
 XX  
 PP 03-NOV-1999; 99WO-CA01029.  
 XX  
 PR 03-NOV-1998; 98US-0185908.  
 PR 30-MAR-1999; 99US-0282029.  
 XX  
 PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
 XX  
 PI Blaschuck OW, Symonds JM, Gour BJ;  
 XX  
 DR WPI; 2000-365610/31.  
 XX  
 PT Antibody modulation of claudin-mediated cell adhesion for increasing  
 PT vasopermeability for delivering drugs to tumors and the nervous system  
 PT and across the skin -  
 XX  
 PS Claim 43; Page 96; 121pp; English.  
 XX  
 CC The present invention relates to the use of peptides as claudin-mediated  
 CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,  
 CC which are membrane glycoproteins involved in cell adhesion. In some  
 CC situations, cell adhesion occurs at abnormal levels, and these peptides  
 CC can be used to modulate these levels, and thus treat autoimmune diseases,  
 CC inflammatory diseases and cancer, and aid wound healing and implant  
 CC adhesion. In addition, they can also be used to facilitate drug delivery  
 CC to the desired target site. The present sequence has a cyclic  
 CC conformation.  
 XX  
 SQ Sequence 10 AA;

AAB06485 Length: 10 January 12, 2004 11:04 Type: P Check: 4174 ..

1 CWRIYSYAGC

```

!!AA SEQUENCE 1.0
ID -AAB06491 standard; peptide; 10 AA.
XX
AC AAB06491;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 498.
XX
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI; 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 43; Page 96; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 10 AA;
AAB06491 Length: 10 January 12, 2004 11:04 Type: P Check: 4192 ..
1 KWR1YSYAGD

```

!!IAA SEQUENCE 1.0  
 ID AAB06497 standard; peptide; 10 AA.  
 AC AAB06497;  
 XX  
 DT 28-SEP-2000 (first entry)  
 XX  
 DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 504.  
 XX  
 KW Claudin-1 modulating agent; cell adhesion recognition sequence;  
 KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
 KW graft rejection; cyclic.  
 XX  
 OS Mammalia.  
 XX  
 PN WO200026360-A1.  
 XX  
 PD 11-MAY-2000.  
 XX  
 XX 03-NOV-1999; 99WO-CA01029.  
 XX  
 PR 03-NOV-1998; 98US-0185908.  
 PR 30-MAR-1999; 99US-0282029.  
 XX  
 PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
 XX  
 PI Blaschuck OW, Symonds JM, Gour BJ;  
 XX  
 DR WPI; 2000-365610/31.  
 XX  
 PT Antibody modulation of claudin-mediated cell adhesion for increasing  
 PT vasopermeability, for delivering drugs to tumors and the nervous system  
 PT and across the skin -  
 XX  
 PS Claim 43; Page 97; 121pp; English.  
 XX  
 CC The present invention relates to the use of peptides as claudin-mediated  
 CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,  
 CC which are membrane glycoproteins involved in cell adhesion. In some  
 CC situations, cell adhesion occurs at abnormal levels, and these peptides  
 CC can be used to modulate these levels, and thus treat autoimmune diseases,  
 CC inflammatory diseases and cancer, and aid wound healing and implant  
 CC adhesion. In addition, they can also be used to facilitate drug delivery  
 CC to the desired target site. The present sequence has a cyclic  
 CC conformation.  
 XX  
 SQ Sequence 10 AA;

AAB06497 Length: 10 January 12, 2004 11:04 Type: P Check: 4202 ..

1 KWR1YSYAGE

!!AA\_SEQUENCE 1.0  
ID AAB06503 standard; peptide; 10 AA.  
XX  
AC AAB06503;  
XX  
DT 28-SEP-2000 (first entry)  
XX  
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 510.  
XX  
KW Claudin-1 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection; cyclic.  
XX  
OS Mammalia.  
XX  
PN WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
XX 03-NOV-1999; 99WO-CA01029.  
XX  
XX 03-NOV-1998; 98US-0185908.  
XX 30-MAR-1999; 99US-0282029.  
XX  
XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
XX Blaschuck OW, Symonds JM, Gour BJ;  
XX  
XX WPI; 2000-365610/31.  
XX  
XX Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
XX Claim 43; Page 97; 121pp; English.  
XX  
XX The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site. The present sequence has a cyclic  
CC conformation.  
XX  
SQ Sequence 10 AA;

AAB06503 Length: 10 January 12, 2004 11:04 Type: P Check: 4255 ..

1 DWR1YSYACK

IIAA	SEQUENCE 1.0	
ID	AAB06509 standard; peptide; 10 AA.	
XX		
AC	AAB06509;	
XX		
DT	28-SEP-2000 (first entry)	
XX		
DE	Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 516.	
XX		
KW	Claudin-1 modulating agent; cell adhesion recognition sequence;	
KW	CAR sequence; autoimmune disease; inflammatory disease; cancer;	
KW	graft rejection; cyclic.	
XX		
OS	Mammalia.	
XX		
PN	WO200026360-A1.	
XX		
PD	11-MAY-2000.	
XX		
PF	03-NOV-1999; 99WO-CA01029.	
XX		
PR	03-NOV-1998; 98US-0185908.	
PR	30-MAR-1999; 99US-0282029.	
XX		
PA	(ADHE-) ADHEREX TECHNOLOGIES INC.	
XX		
PI	Blaschuck OW, Symonds JM, Gour BJ;	
XX		
DR	WPI; 2000-365610/31.	
XX		
PT	Antibody modulation of claudin-mediated cell adhesion for increasing	
PT	vasopermeability, for delivering drugs to tumors and the nervous system	
PT	and across the skin -	
XX		
PS	Claim 43; Page 97; 121pp; English.	
XX		
CC	The present invention relates to the use of peptides as claudin-mediated	
CC	cell adhesion modulators. The claudin-1 group of proteins are cadherins,	
CC	which are membrane glycoproteins involved in cell adhesion. In some	
CC	situations, cell adhesion occurs at abnormal levels, and these peptides	
CC	can be used to modulate these levels, and thus treat autoimmune diseases,	
CC	inflammatory diseases and cancer, and aid wound healing and implant	
CC	adhesion. In addition, they can also be used to facilitate drug delivery	
CC	to the desired target site. The present sequence has a cyclic	
CC	conformation.	
XX		
Sequence	10 AA;	

!!AA SEQUENCE 1.0  
ID -AAB06512 standard; peptide; 8 AA.  
AC AAB06512;  
XX  
DT 28-SEP-2000 (first entry)  
XX  
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 519.  
XX  
KW Claudin-1 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection; cyclic.  
XX  
OS Mammalia.  
XX  
PN WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
XX 03-NOV-1999; 99WO-CA01029.  
XX  
PR 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
XX Blaschuck OW, Symonds JM, Gour BJ;  
PI  
XX WPI; 2000-365610/31.  
DR  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
PS Claim 43; Page 97; 121pp; English.  
XX  
XX The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site. The present sequence has a cyclic  
CC conformation.  
XX  
SQ Sequence 8 AA;

AAB06512 Length: 8 January 12, 2004 11:04 Type: P Check: 2798 ..

1 WRIYSYAG

```

!!AA SEQUENCE 1.0
ID_AAB06521 standard; peptide; 8 AA.
XX
AC AAB06521;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-2 cell adhesion recognition sequence SEQ ID NO: 42.
XX
KW Claudin-2 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI; 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 46; Page 97; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
SQ Sequence 8 AA;

```

AAB06521 Length: 8 January 12, 2004 11:04 Type: P Check: 2954 ..

1 WRTSSYVG

!!AA SEQUENCE 1.0  
ID -AAB06530 standard; peptide; 10 AA.  
AC AAB06530;  
DT 28-SEP-2000 (first entry)  
XX  
DE Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 119.  
XX  
DE Claudin-2 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
XX graft rejection; cyclic.  
XX  
OS Mammalia.  
XX  
PN WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
XX 03-NOV-1999; 99WO-CA01029.  
XX  
PR 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
PI Blaschuck OW, Symonds JM, Gour BJ;  
XX  
DR WPI; 2000-365610/31.  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
PS Claim 49; Page 98; 121pp; English.  
XX  
CC The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site. The present sequence has a cyclic  
CC conformation.  
XX  
SQ Sequence 10 AA;  
AAB06530 Length: 10 January 12, 2004 10:59 Type: P Check: 4356 ..  
1 CWTSSYVGC

!!AA\_SEQUENCE 1.0  
ID AAB06539 standard; peptide; 10 AA.  
XX  
AC AAB06539;  
XX  
DT 28-SEP-2000 (first entry)  
XX  
DE Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 128.  
XX  
KW Claudin-2 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection; cyclic.  
XX  
OS Mammalia.  
XX  
PN WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
PF 03-NOV-1999; 99WO-CA01029.  
XX  
PR 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
PI Blaschuck OW, Symonds JM, Gour BJ;  
XX  
DR WPI; 2000-365610/31.  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
PS Claim 49; Page 98; 121pp; English.  
XX  
CC The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site. The present sequence has a cyclic  
CC conformation.  
XX  
SQ Sequence 10 AA;  
AAB06539 Length: 10 January 12, 2004 10:59 Type: P Check: 4374 ..  
1 KWTSSYVGD

!!AA SEQUENCE 1.0  
 ID -AAB06548 standard; peptide; 10 AA.  
 AC AAB06548;  
 XX DT 28-SEP-2000 (first entry)  
 XX DE Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 137.  
 XX DE Claudin-2 modulating agent; cell adhesion recognition sequence;  
 KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
 KW graft rejection; cyclic.  
 XX OS Mammalia.  
 XX PN WO200026360-A1.  
 XX PD 11-MAY-2000.  
 XX PF 03-NOV-1999; 99WO-CA01029.  
 XX PR 03-NOV-1998; 98US-0185908.  
 PR 30-MAR-1999; 99US-0282029.  
 XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
 XX PI Blaschuck OW, Symonds JM, Gour BJ;  
 XX DR WPI; 2000-365610/31.  
 XX PT Antibody modulation of claudin-mediated cell adhesion for increasing  
 PT vasopermeability, for delivering drugs to tumors and the nervous system  
 PT and across the skin -  
 XX PS Claim 49; Page 98; 121pp; English.  
 XX CC The present invention relates to the use of peptides as claudin-mediated  
 CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,  
 CC which are membrane glycoproteins involved in cell adhesion. In some  
 CC situations, cell adhesion occurs at abnormal levels, and these peptides  
 CC can be used to modulate these levels, and thus treat autoimmune diseases,  
 CC inflammatory diseases and cancer, and aid wound healing and implant  
 CC adhesion. In addition, they can also be used to facilitate drug delivery  
 CC to the desired target site. The present sequence has a cyclic  
 CC conformation.

XX Sequence 10 AA;

AAB06548 Length: 10 January 12, 2004 10:59 Type: P Check: 4384 ..

1 KWTSSYVGE

!!AA SEQUENCE 1.0  
ID -AAB06557 standard; peptide; 10 AA.  
XX  
AC AAB06557;  
XX  
DT 28-SEP-2000 (first entry)  
XX  
DE Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 146.  
XX  
KW Claudin-2 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection; cyclic.  
XX  
OS Mammalia.  
XX  
PN WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
PF 03-NOV-1999; 99WO-CA01029.  
XX  
PR 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
PI Blaschuck OW, Symonds JM, Gour BJ;  
XX  
DR WPI; 2000-365610/31.  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
PS Claim 49; Page 98; 121pp; English.  
XX  
CC The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site. The present sequence has a cyclic  
CC conformation.  
XX  
SQ Sequence 10 AA;  
AAB06557 Length: 10 January 12, 2004 11:00 Type: P Check: 4437 ..  
1 DWTSSYVGK

```

!!AA SEQUENCE 1.0
ID AAB06566 standard; peptide; 10 AA.
XX
AC AAB06566;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 155.
XX
DE Claudin-2 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PP 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI; 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 49; Page 98; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 10 AA;

```

AAB06566 Length: 10 January 12, 2004 11:00 Type: P Check: 4438 ..

1 EWTSSYVGK

```

!!AA SEQUENCE 1.0
ID AAB06574 standard; peptide; 8 AA.
XX
AC AAB06574;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 163.
XX
DE Claudin-2 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI; 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 49; Page 98; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA;

```

AAB06574 Length: 8 January 12, 2004 11:00 Type: P Check: 2954 ..

1 WRTSSYVG

!!AA SEQUENCE 1.0  
ID -AAB06583 standard; peptide; 8 AA.  
XX AC AAB06583;  
XX DT 28-SEP-2000 (first entry)  
XX DE Claudin-3 cell adhesion recognition sequence SEQ ID NO: 58.  
XX DE  
XX KW Claudin-3 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection.  
XX OS Mammalia.  
XX PN WO200026360-A1.  
XX PD 11-MAY-2000.  
XX PF 03-NOV-1999; 99WO-CA01029.  
XX PR 03-NOV-1998; 98US-0185908.  
XX PR 30-MAR-1999; 99US-0282029.  
XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX PI Blaschuck OW, Symonds JM, Gour BJ;  
XX DR WPI; 2000-365610/31.  
XX PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX PS Claim 52; Page 99; 121pp; English.  
XX CC The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-3 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site.  
XX SQ Sequence 8 AA;

AAB06583 Length: 8 January 12, 2004 11:00 Type: P Check: 2665 ..

1 WRVSAFIG

```

!!AA SEQUENCE 1.0
ID - AAB06592 standard; peptide; 10 AA.
XX
AC AAB06592;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-3 cyclic cell adhesion recognition sequence SEQ ID NO: 225.
XX
KW Claudin-3 modulating agent; cell adhesion recognition sequence;
XX CAR sequence; autoimmune disease; inflammatory disease; cancer;
XX graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
XX 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI; 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 55; Page 99; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-3 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 10 AA;
AAB06592 Length: 10 January 12, 2004 11:00 Type: P Check: 4019 ..
1 CWRVSAFIGC

```

```

!!AA SEQUENCE 1.0
ID -AAB06601 standard; peptide; 10 AA.
XX
AC AAB06601;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-3 cyclic cell adhesion recognition sequence SEQ ID NO: 234.
XX
KW Claudin-3 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI; 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 55; Page 99; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-3 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.

```

SQ Sequence 10 AA;

AAB06601 Length: 10 January 12, 2004 11:00 Type: P Check: 4037 ..

1 KRVSAFIGD

!!AA SEQUENCE 1.0  
ID AAB06610 standard; peptide; 10 AA.  
XX  
AC AAB06610;  
XX  
DT 28-SEP-2000 (first entry)  
XX  
DE Claudin-3 cyclic cell adhesion recognition sequence SEQ ID NO: 243.  
XX  
DE Claudin-3 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection; cyclic.  
XX  
OS Mammalia.  
XX  
PN WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
PP 03-NOV-1999; 99WO-CA01029.  
XX  
PR 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
PI Blaschuck OW, Symonds JM, Gour BJ;  
XX  
DR WPI; 2000-365610/31.  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
PS Claim 55; Page 99; 121pp; English.  
XX  
CC The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-3 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site. The present sequence has a cyclic  
CC conformation.  
XX  
SQ Sequence 10 AA;  
AAB06610 Length: 10 January 12, 2004 11:00 Type: P Check: 4047 ..  
1 KRVSAFIGE

!!AA SEQUENCE 1.0  
ID -AAB06619 standard; peptide; 10 AA.  
XX  
AC AAB06619;  
XX  
DT 28-SEP-2000 (first entry)  
XX  
DE Claudin-3 cyclic cell adhesion recognition sequence SEQ ID NO: 252.  
XX  
DE Claudin-3 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection; cyclic.  
XX  
OS Mammalia.  
XX  
PN WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
XX 03-NOV-1999; 99WO-CA01029.  
XX  
XX 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
XX Blaschuck OW, Symonds JM, Gour BJ;  
XX  
XX WPI; 2000-365610/31.  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
PS Claim 55; Page 100; 121pp; English.  
XX  
XX The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-3 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site. The present sequence has a cyclic  
CC conformation.  
XX  
SQ Sequence 10 AA;

AAB06619 Length: 10 January 12, 2004 11:00 Type: P Check: 4100 ..

1 DWVSAFIGK

!!AA\_SEQUENCE 1.0  
 ID AAB06628 standard; peptide; 10 AA.  
 AC AAB06628;  
 XX  
 DT 28-SEP-2000 (first entry)  
 XX  
 DE Claudin-3 cyclic cell adhesion recognition sequence SEQ ID NO: 261.  
 XX  
 KW Claudin-3 modulating agent; cell adhesion recognition sequence;  
 KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
 KW graft rejection; cyclic.  
 XX  
 OS Mammalia.  
 XX  
 PN WO200026360-A1.  
 XX  
 PD 11-MAY-2000.  
 XX  
 PF 03-NOV-1999; 99WO-CA01029.  
 XX  
 PR 03-NOV-1998; 98US-0185908.  
 PR 30-MAR-1999; 99US-0282029.  
 XX  
 PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
 XX  
 PI Blaschuck OW, Symonds JM, Gour BJ;  
 XX  
 DR WPI; 2000-365610/31.  
 XX  
 PT Antibody modulation of claudin-mediated cell adhesion for increasing  
 PT vasopermeability, for delivering drugs to tumors and the nervous system  
 PT and across the skin -  
 XX  
 PS Claim 55; Page 100; 121pp; English.  
 XX  
 CC The present invention relates to the use of peptides as claudin-mediated  
 CC cell adhesion modulators. The claudin-3 group of proteins are cadherins,  
 CC which are membrane glycoproteins involved in cell adhesion. In some  
 CC situations, cell adhesion occurs at abnormal levels, and these peptides  
 CC can be used to modulate these levels, and thus treat autoimmune diseases,  
 CC inflammatory diseases and cancer, and aid wound healing and implant  
 CC adhesion. In addition, they can also be used to facilitate drug delivery  
 CC to the desired target site. The present sequence has a cyclic  
 CC conformation.  
 XX  
 SQ Sequence 10 AA;

AAB06628 Length: 10 January 12, 2004 11:01 Type: P Check: 4101 ..

1 EWRVSAFIGK

```

!!AA SEQUENCE 1.0
ID AAB06636 standard; peptide; 8 AA.
XX
AC AAB06636;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-3 cyclic cell adhesion recognition sequence SEQ ID NO: 269.
XX
KW Claudin-3 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI; 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 55; Page 100; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-3 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA;

```

AAB06636 Length: 8 January 12, 2004 11:01 Type: P Check: 2665 ..

1 WRVSAPIG

!!AA\_SEQUENCE 1.0  
ID AAB06645 standard; peptide; 8 AA.  
XX  
AC AAB06645;  
XX  
DT 28-SEP-2000 (first entry)  
XX  
DE Claudin-4 cell adhesion recognition sequence SEQ ID NO: 50.  
XX  
KW Claudin-4 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection.  
XX  
XX Mammalia.  
XX  
PN WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
XX 03-NOV-1999; 99WO-CA01029.  
XX  
PR 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
XX Blaeschuck OW, Symonds JM, Gour BJ;  
XX WPI; 2000-365610/31.  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
PS Claim 58; Page 100; 121pp; English.  
XX  
CC The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-4 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site.  
XX  
SQ Sequence 8 AA;

AAB06645 Length: 8 January 12, 2004 11:01 Type: P Check: 2669 ..

1 WRVTAFIG

```

!!AA SEQUENCE 1.0
ID -AAB06654 standard; peptide; 10 AA.
XX
AC AAB06654;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-4 cyclic cell adhesion recognition sequence SEQ ID NO: 172.
XX
DE Claudin-4 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
XX graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-CA01029.
XX
XX 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuck OW, Symonds JM, Gour BJ;
PI
XX WPI; 2000-365610/31.
DR
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX Claim 61; Page 101; 121pp; English.
XX
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-4 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 10 AA;

```

AAB06654 Length: 10 January 12, 2004 11:01 Type: P Check: 4024 ..

1 CWRVTAFIGC

!!AA SEQUENCE 1.0  
ID AAB06663 standard; peptide; 10 AA.  
XX  
AC AAB06663;  
XX  
DT 28-SEP-2000 (first entry)  
XX  
DE Claudin-4 cyclic cell adhesion recognition sequence SEQ ID NO: 181.  
XX  
DE Claudin-4 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection; cyclic.  
XX  
OS Mammalia.  
XX  
PN WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
XX 03-NOV-1999; 99WO-CA01029.  
XX  
XX 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
XX Blaschuck OW, Symonds JM, Gour BJ;  
PI  
XX WPI; 2000-365610/31.  
DR  
XX  
XX Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
XX Claim 61; Page 101; 121pp; English.  
XX  
XX The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-4 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site. The present sequence has a cyclic  
CC conformation.  
XX  
SQ Sequence 10 AA;  
AAB06663 Length: 10 January 12, 2004 11:01 Type: P Check: 4042 ..  
1 KWRVTAFIGD

!!AA SEQUENCE 1.0  
ID AAB06672 standard; peptide; 10 AA.  
XX  
AC AAB06672;  
XX  
DT 28-SEP-2000 (first entry)  
XX  
DE Claudin-4 cyclic cell adhesion recognition sequence SEQ ID NO: 190.  
XX  
KW Claudin-4 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection; cyclic.  
XX  
OS Mammalia.  
XX  
PN WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
XX 03-NOV-1999; 99WO-CA01029.  
XX  
XX 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
XX Blaschuck OW, Symonds JM, Gour BJ;  
PI  
XX  
DR WPI; 2000-365610/31.  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
XX Claim 61; Page 101; 121pp; English.  
XX  
XX The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-4 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site. The present sequence has a cyclic  
CC conformation.  
XX  
SQ Sequence 10 AA;

AAB06672 Length: 10 January 12, 2004 11:01 Type: P Check: 4052 ..

1 KWRVTAFIGE

!!AA SEQUENCE 1.0  
ID AAB06681 standard; peptide; 10 AA.  
XX  
AC AAB06681;  
XX  
DT 28-SEP-2000 (first entry)  
XX  
DE Claudin-4 cyclic cell adhesion recognition sequence SEQ ID NO: 199.  
XX  
KW Claudin-4 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection; cyclic.  
XX  
OS Mammalia.  
XX  
PN WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
PF 03-NOV-1999; 99WO-CA01029.  
XX  
PR 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
PI Blaschuck OW, Symonds JM, Gour BJ;  
XX  
DR WPI; 2000-365610/31.  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
PS Claim 61; Page 101; 121pp; English.  
XX  
CC The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-4 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site. The present sequence has a cyclic  
CC conformation.  
XX  
SQ Sequence 10 AA;

AAB06681 Length: 10 January 12, 2004 11:01 Type: P Check: 4105 ..

1 DWRVTAFIGK

```

!!AA SEQUENCE 1.0
ID AAB06690 standard; peptide; 10 AA.
AC AAB06690;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-4 cyclic cell adhesion recognition sequence SEQ ID NO: 208.
XX
KW Claudin-4 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI; 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 61; Page 101; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-4 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 10 AA;
AAB06690 Length: 10 January 12, 2004 11:02 Type: P Check: 4106 ..
1 EWRVTAFIGK

```

!!AA\_SEQUENCE 1.0  
ID AAB06698 standard; peptide; 8 AA.  
XX AC AAB06698;  
XX DT 28-SEP-2000 (first entry)  
XX DE Claudin-4 cyclic cell adhesion recognition sequence SEQ ID NO: 216.  
XX KW Claudin-4 modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection; cyclic.  
XX OS Mammalia.  
XX PN WO200026360-A1.  
XX PD 11-MAY-2000.  
XX PF 03-NOV-1999; 99WO-CA01029.  
XX PR 03-NOV-1998; 98US-0185908.  
XX PR 30-MAR-1999; 99US-0282029.  
XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX PI Blaschuck OW, Symonds JM, Gour BJ;  
XX DR WPI; 2000-365610/31.  
XX PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX PS Claim 61; Page 101; 121pp; English.  
XX CC The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-4 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site. The present sequence has a cyclic  
CC conformation.  
XX SQ Sequence 8 AA;

AAB06698 Length: 8 January 12, 2004 11:02 Type: P Check: 2669 ..

1 WRVTAFIG

!!AA SEQUENCE 1.0  
ID -AAB06764 standard; peptide; 8 AA.  
AC AAB06764;  
XX 28-SEP-2000 (first entry)  
XX  
DE Claudin-6/9 cell adhesion recognition sequence SEQ ID NO: 335.  
XX  
XX Claudin-6 modulating agent; claudin-9 modulating agent;  
KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;  
KW inflammatory disease; cancer; graft rejection.  
XX  
OS Mammalia.  
XX  
XX WO200026360-A1.  
XX  
XX 11-MAY-2000.  
XX  
XX 03-NOV-1999; 99WO-CA01029.  
XX  
XX 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
XX Blaschuck OW, Symonds JM, Gour BJ;  
PI  
XX WPI; 2000-365610/31.  
DR  
XX Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
PS Claim 70; Page 103; 121pp; English.  
XX  
XX The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins  
CC are adherins, which are membrane glycoproteins involved in cell  
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,  
CC and these peptides can be used to modulate these levels, and thus treat  
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound  
CC healing and implant adhesion. In addition, they can also be used to  
CC facilitate drug delivery to the desired target site.  
XX  
SQ Sequence 8 AA;  
AAB06764 Length: 8 January 12, 2004 11:02 Type: P Check: 2655 ..  
1 WKVTAFIG

!!AA SEQUENCE 1.0  
ID AAB06772 standard; peptide; 10 AA.  
XX  
AC AAB06772;  
XX  
DT 28-SEP-2000 (first entry)  
XX  
DE Claudin-6/9 cyclic cell adhesion recognition sequence SEQ ID NO: 343.  
XX  
KW Claudin-6 modulating agent; claudin-9 modulating agent;  
KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;  
KW inflammatory disease; cancer; graft rejection; cyclic.  
XX  
OS Mammalia.  
XX  
PN WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
PP 03-NOV-1999; 99WO-CA01029.  
XX  
PR 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
PI Blaschuck OW, Symonds JM, Gour BJ;  
XX  
DR WPI; 2000-365610/31.  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
PS Claim 73; Page 103; 121pp; English.  
XX  
CC The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins  
CC are adherins, which are membrane glycoproteins involved in cell  
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,  
CC and these peptides can be used to modulate these levels, and thus treat  
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound  
CC healing and implant adhesion. In addition, they can also be used to  
CC facilitate drug delivery to the desired target site. The present  
CC sequence has a cyclic conformation.  
XX  
SQ Sequence 10 AA;  
AAB06772 Length: 10 January 12, 2004 10:57 Type: P Check: 4003 ..  
1 CWKVTAFIGC

```

!!AA SEQUENCE 1.0
ID -AAB06781 standard; peptide; 10 AA.
XX
AC AAB06781;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-6/9 cyclic cell adhesion recognition sequence SEQ ID NO: 352.
XX
DE Claudin-6 modulating agent; claudin-9 modulating agent;
KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;
KW inflammatory disease; cancer; graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OM, Symonds JM, Gour BJ;
XX
DR WPI; 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 73; Page 104; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
CC are cadherins, which are membrane glycoproteins involved in cell
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,
CC and these peptides can be used to modulate these levels, and thus treat
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound
CC healing and implant adhesion. In addition, they can also be used to
CC facilitate drug delivery to the desired target site. The present
CC sequence has a cyclic conformation.
XX
SQ Sequence 10 AA;

```

AAB06781 Length: 10 January 12, 2004 10:57 Type: P Check: 4021 ..

1 KWKVTAFIGD

```

!!AA SEQUENCE 1.0
ID AAB06789 standard; peptide; 10 AA.
XX
AC AAB06789;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-6/9 cyclic cell adhesion recognition sequence SEQ ID NO: 360.
XX
KW Claudin-6 modulating agent; claudin-9 modulating agent;
XX cell adhesion recognition sequence; CAR sequence; autoimmune disease;
XX inflammatory disease; cancer; graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
XX 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI; 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 73; Page 104; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
CC are adherins, which are membrane glycoproteins involved in cell
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,
CC and these peptides can be used to modulate these levels, and thus treat
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound
CC healing and implant adhesion. In addition, they can also be used to
CC facilitate drug delivery to the desired target site. The present
CC sequence has a cyclic conformation.
XX
SQ Sequence 10 AA;

```

AAB06789 Length: 10 January 12, 2004 10:57 Type: P Check: 4031 ..

1 KWKVTAFIGE

!!AA SEQUENCE 1.0  
ID -AAB06798 standard; peptide; 10 AA.  
XX  
AC AAB06798;  
XX  
DT 28-SEP-2000 (first entry)  
XX  
DE Claudin-6/9 cyclic cell adhesion recognition sequence SEQ ID NO: 369.  
XX  
KW Claudin-6 modulating agent; claudin-9 modulating agent;  
KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;  
XX inflammatory disease; cancer; graft rejection; cyclic.  
OS Mammalia.  
XX  
PN WO200026360-A1.  
XX  
PD 11-MAY-2000.  
XX  
PF 03-NOV-1999; 99WO-CA01029.  
XX  
PR 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
PI Blaschuck OW, Symonds JM, Gour BJ;  
XX  
DR WPI; 2000-365610/31.  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
PS Claim 73; Page 104; 121pp; English.  
XX  
CC The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins  
CC are adherins, which are membrane glycoproteins involved in cell  
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,  
CC and these peptides can be used to modulate these levels, and thus treat  
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound  
CC healing and implant adhesion. In addition, they can also be used to  
CC facilitate drug delivery to the desired target site. The present  
CC sequence has a cyclic conformation.  
XX  
SQ Sequence 10 AA;  
AAB06798 Length: 10 January 12, 2004 10:57 Type: P Check: 4084 ..  
1 DWKVTAFIGK

!!AA\_SEQUENCE 1.0  
 ID AAB06806 standard; peptide; 10 AA.  
 AC AAB06806;  
 XX  
 DT 28-SEP-2000 (first entry)  
 XX  
 DE Claudin-6/9 cyclic cell adhesion recognition sequence SEQ ID NO: 377.  
 XX  
 KW Claudin-6 modulating agent; claudin-9 modulating agent;  
 KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;  
 KW inflammatory disease; cancer; graft rejection; cyclic.  
 XX  
 OS Mammalia.  
 XX  
 PN WO200026360-A1.  
 XX  
 PD 11-MAY-2000.  
 XX  
 PF 03-NOV-1999; 99WO-CA01029.  
 XX  
 PR 03-NOV-1998; 98US-0185908.  
 PR 30-MAR-1999; 99US-0282029.  
 XX  
 PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
 XX  
 PI Blaschuck OW, Symonds JM, Gour BJ;  
 XX  
 DR WPI; 2000-365610/31.  
 XX  
 PT Antibody modulation of claudin-mediated cell adhesion for increasing  
 PT vasopermeability, for delivering drugs to tumors and the nervous system  
 PT and across the skin -  
 XX  
 PS Claim 73; Page 104; 121pp; English.  
 XX  
 CC The present invention relates to the use of peptides as claudin-mediated  
 CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins  
 CC are adherins, which are membrane glycoproteins involved in cell  
 CC adhesion. In some situations, cell adhesion occurs at abnormal levels,  
 CC and these peptides can be used to modulate these levels, and thus treat  
 CC autoimmune diseases, inflammatory diseases and cancer, and aid wound  
 CC healing and implant adhesion. In addition, they can also be used to  
 CC facilitate drug delivery to the desired target site. The present  
 CC sequence has a cyclic conformation.

SQ Sequence 10 AA;

AAB06806 Length: 10 January 12, 2004 10:59 Type: P Check: 4085 ..

1 EMKVTAFIGK

```

!!AA SEQUENCE 1.0
ID -AAB06814 standard; peptide; 8 AA.
XX
AC AAB06814;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-6/9 cyclic cell adhesion recognition sequence SEQ ID NO: 385.
XX
DE Claudin-6 modulating agent; claudin-9 modulating agent;
XX cell adhesion recognition sequence; CAR sequence; autoimmune disease;
XX inflammatory disease; cancer; graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO2000026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
XX 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI; 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 73; Page 104; 121pp; English.
XX
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
CC are adherins, which are membrane glycoproteins involved in cell
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,
CC and these peptides can be used to modulate these levels, and thus treat
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound
CC healing and implant adhesion. In addition, they can also be used to
CC facilitate drug delivery to the desired target site. The present
CC sequence has a cyclic conformation.
XX
SQ Sequence 8 AA;

```

AAB06814 Length: 8 January 12, 2004 10:59 Type: P Check: 2655 ..

1 WKVTAFIG

!!AA SEQUENCE 1.0  
ID AAB06911 standard; Protein; 10 AA.  
XX  
AC AAB06911;  
XX  
DT 05-OCT-2000 (first entry)  
XX  
DE Claudin cell adhesion recognition modulating sequence SEQ ID NO: 475.  
XX  
DE Claudin modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /note= "N-terminal acetyl or hydrogen"  
FT Modified-site 10 /note= "C-terminal amide"  
FT  
XX WO200026360-A1.  
PN  
XX  
PD 11-MAY-2000.  
XX  
PF 03-NOV-1999; 99WO-CA01029.  
XX  
PR 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
PI Blaschuck OW, Symonds JM, Gour BJ;  
XX  
DR WPI; 2000-365610/31.  
XX  
PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
PS Disclosure; Page 19; 121pp; English.  
XX  
CC The present sequence is a peptide which can be used in a claudin-mediated  
CC cell adhesion modulator. The claudin group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and this peptide  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, it can also be used to facilitate drug delivery  
CC to the desired target site.  
XX  
SQ Sequence 10 AA;  
AAB06911 Length: 10 January 12, 2004 10:59 Type: P Check: 4176 ..  
1 WKIYSYAGDN

!!AA SEQUENCE 1.0  
ID AAB06916 standard; Protein; 8 AA.  
XX  
AC AAB06916;  
XX  
DT 05-OCT-2000 (first entry)  
XX  
DE Claudin cell adhesion recognition modulating sequence SEQ ID NO: 50.  
XX  
DE Claudin modulating agent; cell adhesion recognition sequence;  
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
KW graft rejection.  
XX  
OS Synthetic.  
XX  
XX  
PH Key Location/Qualifiers  
FT Modified-site 1 /note= "N-terminal acetyl"  
FT Modified-site 8  
FT Modified-site 8 /note= "C-terminal amide"  
XX  
XX WO200026360-A1.  
XX  
XX 11-MAY-2000.  
XX  
XX 03-NOV-1999; 99WO-CA01029.  
XX  
XX 03-NOV-1998; 98US-0185908.  
PR 30-MAR-1999; 99US-0282029.  
XX  
XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
XX Blaschuck OW, Symonds JM, Gour BJ;  
PI  
XX WPI; 2000-365610/31.  
XX  
XX Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin -  
XX  
XX Claim 71; Page 103; 121pp; English.  
XX  
XX The present sequence is a peptide which can be used in a claudin-mediated  
CC cell adhesion modulator. The claudin group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and this peptide  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, it can also be used to facilitate drug delivery  
CC to the desired target site.  
XX  
SQ Sequence 8 AA;  
AAB06916 Length: 8 January 12, 2004 10:59 Type: P Check: 2655 ..  
1 WKYTAFIC

!!AA SEQUENCE 1.0  
ID - AAB71661 standard; protein; 41 AA.  
XX  
AC AAB71661;  
XX  
DT 10-MAY-2001 (first entry)  
XX  
DE Human colon associated protein #9.  
XX  
KW Human; colon; cancer; disease.  
XX  
OS Homo sapiens.  
XX  
PN WO200112781-A1.  
XX  
PD 22-FEB-2001.  
XX  
PF 11-AUG-2000; 2000MO-US22157.  
XX  
PR 13-AUG-1999; 99US-0148680.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Birse CE, Rosen CA;  
XX  
WP 2001-147551/15.  
XX  
PT Nucleic acids encoding 13 human colon cancer associated polypeptides,  
PT useful for preventing, diagnosing and/or treating e.g. cancers  
PT (especially colon cancer), Parkinson's disease and diabetic retinopathy  
PT -  
XX  
Claim 11; Page 320-321; 326pp; English.  
XX  
CC The present invention relates to 13 human colon cancer-associated  
CC proteins. These proteins and the nucleic acid encoding them may be  
CC used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate colon cancer-associated protein  
CC expression.  
XX  
SQ Sequence 41 AA;  
AAB71661 Length: 41 January 12, 2004 10:54 Type: P Check: 6573 ..  
1 MTGAGLGRDS GRWREVSFFG ETERARGGTV GRGRLRRQ E

!!AA SEQUENCE 1.0  
ID -AAU43488 standard; Protein; 50 AA.  
XX AC AAU43488;  
XX DT 27-FEB-2002 (first entry)  
XX DE Propionibacterium acnes immunogenic protein #4384.  
XX KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;  
XX KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;  
XX KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;  
XX KW dermatological; osteopathic; neuroprotectant.  
XX OS Propionibacterium acnes.  
XX PN WO200181581-A2.  
XX PD 01-NOV-2001.  
XX PF 20-APR-2001; 2001WO-US12865.  
XX PR 21-APR-2000; 2000US-199047P.  
XX PR 02-JUN-2000; 2000US-208841P.  
XX PR 07-JUL-2000; 2000US-216747P.  
XX PA (CORI-) CORIXA CORP.  
XX PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;  
XX PI L'maisonneuve J, Zhang Y, Jen S, Carter D;  
XX DR WPI; 2001-616774/71.  
XX DR N-PSDB; AAS59520.  
XX PT Propionibacterium acnes polypeptides and nucleic acids useful for  
XX PT vaccinating against and diagnosing infections, especially useful for  
XX PT treating acne vulgaris .  
XX PS Example 1; SEQ ID No 4683; 1069pp; English.  
XX CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic  
XX CC polypeptides. The proteins and their associated DNA sequences are used in  
XX CC the treatment, prevention and diagnosis of medical conditions caused by  
XX CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,  
XX CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.  
XX CC P. acnes is also involved in infections of bone, joints and the central  
XX CC nervous system, however it is particularly involved in the inflammatory  
XX CC lesions associated with acne vulgaris. A method for detecting the  
XX CC presence or absence of P. acnes in a patient comprises contacting a  
XX CC sample with a binding agent that binds to the proteins of the invention  
XX CC and determining the amount of bound protein in the sample. The  
XX CC polypeptides may be used as antigens in the production of antibodies  
XX CC specific for P. acnes proteins. These antibodies can be used to  
XX CC downregulate expression and activity of P. acnes polypeptides and  
XX CC therefore treat P. acnes infections. The antibodies may also be used as  
XX CC diagnostic agents for determining P. acnes presence, for example, by  
XX CC enzyme linked immunosorbent assay (ELISA).  
XX CC Note: The sequence data for this patent did not form part of the printed  
XX CC specification, but was obtained in electronic format directly from WIPO  
XX CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX SQ Sequence 50 AA;  
AAU43488 Length: 50 January 12, 2004 10:56 Type: P Check: 1666 ..  
1 WRPGSSWRP WAFRGSSTTR SSLRCLRTG QSCFPSSVQR WLSLRWARSS

!!AA SEQUENCE 1.0  
ID ABB56595 standard; Peptide; 14 AA.  
XX AC ABB56595;  
XX DT 05-MAR-2002 (first entry)  
XX DE Human SNP related amino acid sequence SEQ ID NO:1160.  
XX KW Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;  
KW immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;  
KW autoimmune disease; inflammation; cancer; nervous system disease;  
KW infection; polymorphic protein.  
XX OS Homo sapiens.  
XX PN WO200138586-A2.  
XX PD 31-MAY-2001.  
XX PF 22-NOV-2000; 2000WO-US32311.  
XX PR 24-NOV-1999; 99US-0167383.  
XX PA (CURA-) CURAGEN CORP.  
XX PI Shimkets RA, Leach M;  
XX DR WPI; 2001-355949/37.  
XX PT Isolated human nucleic acids comprising one or more single nucleotide  
PT polymorphisms, useful for treating a subject suffering from a  
PT pathology, e.g. autoimmune diseases, ascribed to the presence of a  
PT sequence polymorphism -  
XX Claim 1; Page 599; 674pp; English.  
XX ABL00010 to ABL01104 represent human nucleic acid oligonucleotides  
CC comprising one or more single nucleotide polymorphisms (SNPs). ABB56531  
CC to ABB56903 represent human peptides encoded by some of the SNP  
CC oligonucleotides. The sequences from the present invention can have  
CC immunosuppressive, cytostatic, antiinflammatory, neuroprotective and  
CC antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides  
CC and antibodies from the present invention can be used for treating a  
CC subject suffering from, at risk for, or suspected of, suffering from a  
CC pathology ascribed to the presence of a sequence polymorphism. The  
CC pathology may be autoimmune diseases, inflammation, cancer, diseases of  
CC the nervous system, and infection by pathogenic microorganisms. The SNPs  
CC are also useful for determining which forms of a characterised  
CC polymorphism are present in individuals. The antibodies may be used in  
CC the detection, quantitation and/or cellular or tissue localisation of a  
CC polymorphic protein (e.g., for use in measuring levels of the  
CC polymorphic protein within appropriate physiological samples).  
XX SQ Sequence 14 AA;

ABB56595 Length: 14 January 12, 2004 10:55 Type: P Check: 8381 ..

1 MLLPSMRTSS YVGA

```

!!AA SEQUENCE 1.0
ID -ABB81045 standard; peptide; 8 AA.
XX
AC ABB81045;
XX
DT 05-NOV-2002 (first entry)
XX
DE Fab fragment directed against claudin CAR sequence.
XX
KW JAM; CAR, junctional adhesion molecule; cell adhesion; drug delivery;
KW angiogenesis; tumour; graft; transplant; wound; claudin.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 8
FT /note= "C-terminal amide"
XX
PN US6391855-B1.
XX
PD 21-MAY-2002.
XX
PF 02-JUN-1999; 99US-0324541.
XX
PR 02-JUN-1999; 99US-0324541.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuk OW, Symonds JM, Gour BJ;
XX
DR WPI; 2002-546108/58.
XX
PT Modulating agents for enhancing or inhibiting the action of junctional
PT adhesion molecule-mediated cell adhesion, useful in drug delivery,
PT anti-cancer treatment and wound repair -
XX
PS Disclosure; Column 32; 26pp; English.
XX
CC The invention provides modulating agents for enhancing or inhibiting the
CC action of junctional adhesion molecule (JAM)-mediated cell adhesion. The
CC cell adhesion modulating agent comprises : (a) at least five consecutive
CC amino acids of a JAM cell adhesion recognition (CAR) sequence as shown in
CC ABB81035 and (b) no more than 50 consecutive amino acid residues linked
CC by peptide bonds. The agents are useful in a wide variety of applications
CC including enhanced transdermal drug delivery, inhibition of angiogenesis,
CC inhibition of cell adhesion in tumours, increased healing of grafts,
CC transplants and wounds and in assessing the efficacy of other modulating
CC agents for JAM. The present sequence represents a Fab fragment directed
CC against claudin CAR sequence.
XX
SQ Sequence 8 AA;

```

ABB81045 Length: 8 January 12, 2004 10:57 Type: P Check: 2784 ..

1 WKIYSYAG

!!AA SEQUENCE 1.0  
ID ABP53938 standard; peptide; 9 AA.  
XX  
AC ABP53938;  
XX  
DT 09-JAN-2003 (first entry)  
XX  
VEGFR-3 binding peptide SEQ ID NO:41.  
XX  
XX Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;  
KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;  
KW cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;  
KW vulnary; cell surface receptor; cancer; neovascularisation;  
KW liver disease; hypertension; post-trauma; chronic hepatitis;  
KW haemangioma; diabetes; PDGF; platelet derived growth factor.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200257299-A2.  
XX  
PD 25-JUL-2002.  
XX  
PF 16-JAN-2002; 2002WO-IB00099.  
XX  
PR 17-JAN-2001; 2001US-262476P.  
XX  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN ) LICENTIA LTD.  
XX  
PI Alitalo K, Koivunen E, Kubo H;  
XX  
DR WPI; 2002-691521/74.  
XX  
PT New isolated peptide that inhibits VEGF-C and VEGF-D, useful for  
PT diagnosing, evaluating, treating disorders mediated by VEGFR-3  
PT activity, such as cancer and diseases of neovascularization -  
XX  
PS Claim 14; Page 80; 149pp; English.  
XX  
CC The present invention describes an isolated peptide (I) that binds to  
CC and inhibits vascular endothelial growth factor receptor 3 (VEGFR-3).  
CC (I) have cytostatic, hepatotropic, antiinflammatory, hypotensive,  
CC antidiabetic and vulnary activities, and can be used in gene therapy.  
CC Compositions and methods from the present invention are useful for  
CC diagnosing, evaluating and treating disorders mediated by the activity  
CC of the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,  
CC liver, spleen, kidney, lymph node, small intestine, blood cells,  
CC pancreas, colon, stomach, breast, endometrium, prostate, testicle,  
CC ovary, skin, head and neck, oesophagus, bone, marrow or blood, and  
CC diseases of neovascularisation, e.g. liver diseases, hypertension,  
CC post-trauma, chronic hepatitis, haemangiomas and diabetes. The present  
CC sequence represents a specifically claimed VEGFR-3 binding peptide from  
CC the present invention.  
XX  
SQ Sequence 9 AA;

ABP53938 Length: 9 January 12, 2004 10:56 Type: P Check: 3468 ..

1 RWRGNAYPG